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OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 04:55:04 ; Search time 400 Seconds
(without alignments)
1858.587 Million cell updates/sec

Title: US-09-808-388-5_COPY_1_175

Perfect score: 175

Sequence: 1 cgcggcaaaactgctgaaa.....tccccagccttgctgcctac 175

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_29Jan04.*

- 1: geneseqn1980s.*
- 2: geneseqn1990s.*
- 3: geneseqn2000s.*
- 4: geneseqn2001as.*
- 5: geneseqn2001bs.*
- 6: geneseqn2002s.*
- 7: geneseqn2003as.*
- 8: geneseqn2003bs.*
- 9: geneseqn2003cs.*
- 10: geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	175	100.0	271	4	Aa164307 Partial h
2	175	100.0	332	4	Aa164308 Partial s
3	171.4	97.9	1116	2	Aa241274 Human nor
4	171.4	97.9	6172	1	Aa91825 HindIII f
5	128	73.1	1080	1	Aa91259 Nucleotid
6	128	73.1	1080	7	ACC46920 Human pho
7	110.8	63.3	5356	6	ABL70442 Chemical
8	110.8	63.3	5728	6	ABK31473 Signal tr
9	110.8	63.3	6083	4	AAS46715 Tumour su
10	94.8	54.2	5356	6	AB170441 Chemical
11	94.8	54.2	5728	6	ABK31472 Signal tr
12	94.8	54.2	6083	4	AAS46714 Tumour su
13	47	26.9	3330	6	ABK63588 Rat sequ
14	47	26.9	3330	7	ABT42455 Toxicity
15	47	26.9	3330	9	ADB59181 Toxicity-
16	44.4	25.4	4990	7	ACC47000 Mouse pho
17	31.2	17.8	420	3	AAC61755 cDNA enco
18	31.2	17.8	1441	3	AAC61753 cDNA enco
19	31.2	17.8	2236	3	AAC61749 cDNA enco
20	31.2	17.8	2307	6	AB211921 Human pol
21	31.2	17.8	2604	3	AAC61758 cDNA enco
22	31.2	17.8	2701	3	AAC61747 cDNA enco
23	31.2	17.8	3320	6	ABA05868 Human lip

24	31.2	17.8	3320	9	AAD60556 Human lip
25	31.2	17.8	3384	3	AAC61761 cDNA enco
26	30.8	17.6	2368	4	AAS41588 cDNA enco
27	30.8	17.6	2735	4	AAS41048 cDNA enco
28	30.6	17.5	305	3	AZ280534 Human col
29	30.6	17.5	2433	2	AAT29396 Apoptosis
30	30.6	17.5	2856	6	ABK92173 Prostate
31	30.6	17.5	2856	9	ACF79927 Breast ca
32	30.6	17.5	2885	6	ABN96891 Gene #338
33	30.6	17.5	2885	7	ACA56545 Human sig
34	30.6	17.5	2885	7	ADA05885 Human NOV
35	30.6	17.5	3370	7	ABX63339 Human cDN
36	30.4	17.4	1549	2	AZ22842 Human zin
37	30.4	17.4	2835	9	ADB63347 Human cDN
38	30.2	17.3	499	8	ACH33946 Human end
39	30.2	17.3	669	4	AAS30751 Human cDN
40	30.2	17.3	1004	4	AAS33189 DNA encod
41	30.2	17.3	1022	4	AAS33069 DNA encod
42	30.2	17.3	1038	4	AAS33340 DNA encod
43	30.2	17.3	1082	6	ABQ55033 Human ova
44	30.2	17.3	1190	4	AAS33153 DNA encod
45	30.2	17.3	1227	4	AAS33320 DNA encod

ALIGNMENTS

RESULT 1

AAI64307
ID AAI64307 standard; DNA; 271 BP.

XX
AC AAI64307;

XX
DT 15-NOV-2001 (first entry)

XX
DE Partial human PLA2SIIA gene promoter.

XX
KW PPAR response element; antiinflammatory; antiarthritic; cytostatic;
cardiant; nootropic; promoter; arthritis; tumour; PLA2SIIA;
KW peroxisome proliferator activated receptor; human;
secreted non-pancreatic phospholipase A2; ds.

XX
OS Homo sapiens.

XX
FN WO200168845-A2.

XX
PD 20-SEP-2001.

XX
PF 14-MAR-2001; 2001WO-FR000759.

XX
PR 14-MAR-2000; 2000FR-00003262.

XX
PA 13-APR-2000; 2000US-0196959P.

XX
(AVET) AVENTIS PHARMA SA.

XX
PI Massaad C, Berenbaum F, Olivier J, Salvat C, Bereziat G;

XX
WPI; 2001-582451/65.

XX
DR New hybrid promoter induced by inflammation, useful in gene therapy of
arthritis, comprises peroxisome proliferator activated receptor response
element and promoter of secreted phospholipase A2.

XX
PS Claim 5; Page 51; 52pp; French.

XX
CC The present invention relates to a hybrid promoter comprising (i) a PPAR
(peroxisome proliferator activated receptor) response element (PPRE); and
(ii) at least part of the promoter of the PLA2SIIA (secreted non-
pancreatic phospholipase A2) gene. The hybrid promoter can be used to
regulate expression of therapeutic transgenes for experimental,
clinical, therapeutic or diagnostic use, especially in chondrocytes for
treatment of arthritis, but also in bone, muscle, liver, heart, the
nervous system and tumours. The present sequence is a partial human

09/808,388
EXAMINER'S SEARCH NOTES
9/24/2004

CC PLA2sIIA promoter sequence, which was used to generate the hybrid
 CC promoter of the present invention
 XX
 SQ Sequence 271 BP; 70 A; 79 C; 71 G; 51 T; 0 U; 0 Other;
 Query Match 100.0%; Score 175; DB 4; Length 271;
 Best Local Similarity 100.0%; Pred. No. 6.4e-50;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCGCGCAAAACCTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAA 60
 Db 1 CCGCGCAAAACCTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAA 60
 QY 61 TCCTCAACTCTCTGCTGCCAGCTGATGAGGGGAAGAAAGGATTACCTAGGGGTATGG 120
 Db 61 TCCTCAACTCTGCTGCCAGCTGATGAGGGGAAGAAAGGATTACCTAGGGGTATGG 120
 QY 121 CGACCAATCTGAGTCCCAACTGACACGCGGCCATCCCGAGCCTTGTCCTCAC 175
 Db 121 CGACCAATCTGAGTCCCAACTGACACGCGGCCATCCCGAGCCTTGTCCTCAC 175

RESULT 2
 AAI64308
 ID AAI64308 standard; DNA; 332 BP.
 XX
 AC AAI64308;
 XX
 DT 15-NOV-2001 (first entry)
 XX
 DE Partial synthetic PLA2sIIA gene promoter.
 XX
 KW PPAR response element; antiinflammatory; antiarthritic; cytostatic;
 KW cardiant; nootropic; promoter; arthritis; tumour; PLA2sIIA;
 KW peroxisome proliferator activated receptor;
 KW secreted non-pancreatic phospholipase A2; ds.
 XX
 OS Synthetic.
 XX
 XX WO200168845-A2.
 XX
 XX 20-SEP-2001.
 XX
 XX 14-MAR-2001; 2001WO-FR000759.
 XX
 XX 14-MAR-2000; 2000FR-00003262.
 PR
 PR 13-APR-2000; 2000US-0196959P.
 XX
 XX (AVET) AVENTIS PHARMA SA.
 PA

Massaad C, Berenbaum F, Olivier J, Salvat C, Bereziat G;
 WPI; 2001-582451/65.
 New hybrid promoter induced by inflammation, useful in gene therapy of
 arthritis, comprises peroxisome proliferator activated receptor response
 element and promoter of secreted phospholipase A2.
 XX
 XX Disclosure; Page 51-52; 52pp; French.
 XX
 XX The present invention relates to a hybrid promoter comprising (i) a PPAR
 CC (peroxisome proliferator activated receptor) response element (PPRE); and
 CC (ii) at least part of the promoter of the PLA2sIIA (secreted non-
 CC pancreatic phospholipase A2) gene. The hybrid promoter can be used to
 CC regulate expression of therapeutic transgenes, for experimental,
 CC clinical, therapeutic or diagnostic use, especially in chondrocytes for
 CC treatment of arthritis, but also in bone, muscle, liver, heart, the
 CC nervous system and tumours. The present sequence is a partial synthetic
 CC PLA2sIIA promoter sequence, which was used to generate the hybrid
 CC promoter of the present invention
 XX
 SQ Sequence 332 BP; 96 A; 91 C; 82 G; 63 T; 0 U; 0 Other;

Query Match 100.0%; Score 175; DB 4; Length 332;
 Best Local Similarity 100.0%; Pred. No. 6.9e-50;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCGCGCAAAACCTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAA 60
 Db 62 CCGCGCAAAACCTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAA 121
 QY 61 TCCTCAACTCTCTGCTGCCAGCTGATGAGGGGAAGAAAGGATTACCTAGGGGTATGG 120
 Db 122 TCCTCAACTCTCTGCTGCCAGCTGATGAGGGGAAGAAAGGATTACCTAGGGGTATGG 181
 QY 121 CGACCAATCTGAGTCCCAACTGACACGCGGCCATCCCGAGCCTTGTCCTCAC 175
 Db 182 CGACCAATCTGAGTCCCAACTGACACGCGGCCATCCCGAGCCTTGTCCTCAC 236

RESULT 3
 AA241274
 ID AA241274 standard; cDNA; 1116 BP.
 XX
 AC AA241274;
 XX
 DT 18-JAN-2000 (first entry)
 XX
 DE Human normal ovarian tissue derived cDNA 53.
 DE
 XX Human; ovary; screening; ovarian cancer; treatment; ss.
 XX
 KW Homo sapiens.
 OS
 XX DE19816395-A1.
 PN
 XX 07-OCT-1999.
 PD
 XX 03-APR-1998; 98DE-01016395.
 PF
 XX 03-APR-1998; 98DE-01016395.
 PR
 XX (META-) METAGEN GES GENOMFORSCHUNG MBH.
 PA
 XX Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl B;
 PI
 PI WPI; 1999-552352/47.
 XX
 DR Nucleic acid sequences potentially useful in diagnosis or therapy of
 XX ovarian cancer.
 PT
 PT Claim 3; Page 164; 274pp; German.
 XX
 PS This invention describes novel nucleic acid sequences that are highly
 CC expressed in normal ovary tissue. Artificial chromosomes and cosmid
 CC clones containing the sequences can be used as gene transfer vehicles.
 CC The sequences can be used to produce DNA fragments containing full-length
 CC genes. Host cells transformed with the sequences can be used to produce
 CC polypeptides or polypeptide fragments, which can be used to screen phage
 CC displays for polypeptides that bind to them, or as tools for identifying
 CC agents active against ovarian cancer, or to prepare medicaments for
 CC treating ovarian cancer. The cDNA sequences can be used to obtain genomic
 CC genes, their promoters, enhancers, silencers, exon structures, intron
 CC structures and their splice variants. AA241222-241324 represent cDNA
 CC sequences derived from normal human ovarian tissue and which encode the
 CC protein fragments represented in AA259724-V59837
 CC
 XX Sequence 1116 BP; 311 A; 311 C; 266 G; 228 T; 0 U; 0 Other;
 SQ

Query Match 97.9%; Score 171.4; DB 2; Length 1116;
 Best Local Similarity 99.4%; Pred. No. 1.8e-48;
 Matches 172; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 CCGCAAAACCTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAATC 62
 Db 6 CTGCAAAACCTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAATC 65

CC contains 5 copies of the X chromosome (GM5009). The plaques were screened
CC for a gene encoding PUA2 using probes designed from peptides derived from
CC the purified protein. A positive clone, PUA2 8.5 EMBL3 was purified and a
CC 6.2 kb insert sequenced (shown here). Corresponding cDNA sequences (i.e.
CC without introns; see N97209) can be ligated into expression vectors for
CC the prodn. of recombinant PUA2. The protein, and antibodies raised to it,
CC can be used for diagnosis of inflammation and tissue injury associated
CC with various diseases. See also N91826-33 and N97209. (Updated on 25-MAR-
CC 2003 to correct PR field.)

QY	63	CTCAACTCTGTCCTGCCAGCTGATGAGGGGAAGAAAGGATTACTTAGGGGTATGGGG	122
Db	66	CTCAACTCTGTCCTGCCAGCTGATGAGGGGAAGAAAGGATTACTTAGGGGTATGGGG	125
QY	123	ACCAATCCTGAGTCCACCAACTGACCAACGGCCATCCCCAGCCCTTGTCCTCAC	175
Db	126	ACCAATCCTGAGTCCACCAACTGACCAACGGCCATCCCCAGCCCTTGTCCTCAC	178

Seq	Sequence	6172 BP;	1624 A;	1408 C;	1740 G;	1400 T;	0 U;	0 Other;
	Query Match	97.9%	Score	171.4;	DB 1;	Length	6172;	
	Best Local Similarity	99.4%;	Pred. No.	3.4e-48;				
	Matches	172;	Conservative	0;	Mismatches	1;	Indels	0;
	Gaps	0;						
Qy	3	CGGC	AAACTCTGCT	GAATGTTGTTTGGCATCAGCTACTCAGACGTAAAGTTTCCCAATC	62			
Db	1378	CTGCA	AAACTGCGCTGAATGTTTGGCATCAGCTACTCAGACGTAAAGTTTCCCAATC	1437				
Qy	63	CTCAACTCTCTCTCGCCAGCTGATGAGGGGAAAGGAAAGGATTACCTAGGGGTATGGCG	122					
Db	1438	CTCAACTCTCTCTCGCCAGCTGATGAGGGGAAAGGAAAGGATTACCTAGGGGTATGGCG	1497					
Qy	123	ACCAATCTGAGTCCACCAACTGACCAACGCCCATCCCGACCTTGTCCTCAC	175					
Db	1498	ACCAATCTGAGTCCACCAACTGACCAACGCCCATCCCGACCTTGTCCTCAC	1550					

RESULT 4	
AAN91825	
ID	AAN91825 standard; DNA; 6172 Bp.
XX	
XX	
AC	AAN91825;
XX	
XX	
25-MAR-2003	(revised)
DT	
31-JUL-1992	(first entry)
DT	
XX	
XX	
HindIII	fragment of PLA2 8.5 EMBL3 encoding human inflammatory phospholipase A2.
DE	
DE	
XX	
XX	
KW	Inflammation; acid stable; phosphatide 2-acylhydrolase; lipolytic;
KW	glycerophospholipids; non-pancreatic; ss.

Key	Location/Qualifiers
AAAN91259	889..893
ID	AAAN91259 standard; DNA; 1080 BP.
XX	
AC	AAAN91259;
XX	
DT	25-MAR-2003 (revised)
DT	27-JUN-1980 (first entry)
XX	
DE	Nucleotide sequence of exon 1 from genomic clone lambda sPLA2-6 of human synovial phospholipase 2 (sPLA2) type A.
DE	
XX	
KW	Human synovial phospholipase A2 gene; clone lambda sPLA2-6; exon 1.
XX	
OS	Homo sapiens.
XX	
PH	
Key	Location/Qualifiers
FT	CAAT_signal
FT	889..893
FT	/*tag= a
FT	968..974
FT	TATA_signal
FT	/*tag= b
FT	1016..1035
FT	exon
FT	/*tag= c
FT	/*note= "Exon 1"

```
FT      exon          1..2492
FT      FT           /tag= a
FT      FT           /number= 1
FT      sig_peptide  2453..2721
FT      FT           /tag= e
FT      exon         2702..2846
FT      FT           /tag= b
FT      FT           /number= 2
FT      misc_feature 2715..2826
FT      FT           /tag= g
FT      FT           /note= "Claim 24"
FT      misc_feature 2715..2826
FT      FT           /tag= g
FT      FT           /note= "Claim 24"
FT      exon         3105..3211
FT      FT           /tag= c
FT      FT           /number= 3
FT      exon         5383..6172
FT      FT           /tag= d
FT      FT           /number= 4
FT      polyA_signal 5771..5776
FT      FT           /tag= f
```

XX	WO8901773-A.	
PN		
XX	09-MAR-1989.	
XX		
XX	23-AUG-1988;	88WO-US002896.
XX		
XX	27-AUG-1987;	87US-00089883.
PR		
PR	06-JUL-1988;	88US-00215726.
PR	16-AUG-1988;	88US-00231865.
XX		
XX	(BIOT-) BIOTECHN RES PARTN.	
PA	(UTOR) UNIV OF TORONTO INNOVAT.	
PA		
XX		
XX	Johnson LK, Seilhamer JJ, Pruzanski W, Vadas P;	
PI		
XX		
XX	WPI; 1989-085394/11.	
DR		
XX		
XX	Mammalian synovial phospholipase A2 - used in food processing, design and	
PT	screening of inflammation inhibitors, as an anticancer drug or vaccine	

PD	19-001-1989.	
XX		
PF	11-APR-1989;	89WO-US001418.
XX		
XX	15-APR-1988;	88US-00181893.
PR	12-JUL-1988;	88US-00219491.
XX		
XX		
PA	(BIOJ) BIOGEN INC.	
XX		
PI	Kramer RM,	Pepinsky R, Hession C;
XX		
XX	WPI; 1989-324225/44.	
DR	P-PSDB; AAP93112.	
XX		
XX		
PT	Acid stable phospholipase A2 - used for prodn. of antibodies and in the treatment or diagnosis of inflammation and other diseases.	
XX		
XX		
PS	Claim 27; Fig 12; 84pp; English.	
XX		
CC	A genomic DNA library was prepod. from a mutant fibroblast cell line which	

PT adjuvant etc.

XX Fig 7; Page ?; 70pp; English.

XX EMBL3-human leucocyte genomic library was screened using labelled probes

CC (n90885 and n90887) based on sPLA2. Clone lambda SPLA2-6 is one of the

CC two unique sPLA2 clones thus identified. SPLA2-6 exons were identified

CC using the cDNA sequence in lambda SPLA2cDNA-4 (n91258). There are five

CC exons in lambda SPLA2-6. This is the first one. The other four are in

CC n91260. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-

CC 2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)

XX

XX Sequence 1080 BP; 306 A; 242 C; 303 G; 229 T; 0 U; 0 Other;

SQ

Query Match 73.1%; Score 128; DB 1; Length 1080;

Best Local Similarity 89.9%; Pred. No. 1.5e-33;

Matches 160; Conservative 0; Mismatches 15; Indels 3; Gaps 2;

QY 1 CGCGGCAAAACCTGCTGAATGCTTTGGCATCAGCTACTGACACGTAAG-GGTTTCCCA 59

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

763 CTCGGCAAAACCTGCTGAATGCTTTGGCATCAGCTACTGACACGTAAGGGTTTCCCA 822

QY 60 ATCTCTCAACTCTGTCTCTG--CCAGCTGATGAGGGGAAGAAAGGATTACCTAGGGGTAT 117

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

823 ATCTCTCAACTCTGTCTCTGCGCAGGCTGATGAGGGGAAGAAAGGATTACCTAGGGGTAT 882

QY 118 GGGCGACCAATCCTGAGTCCCACTGACACGCGCCATCCCGAGCTTGTGCCTCAC 175

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

883 GGGCGACCAATCCTGAGTCCCACTGACACGCGCCATCCCGAGCTTGTGCCTCAC 940

RESULT 6

ABL70442/c

ID ABL70442 standard; DNA; 1080 BP.

XX

AC ACC46920;

XX

DT 05-JUN-2003 (first entry)

XX

DE Human phospholipase A2 group IIA (synovial) nucleotide sequence SEQ.17.

XX

KW Phospholipase A2 group IIA; synovial; antisense modulation; inflammation;

KW phospholipase A2 group IIA inhibitor; phosphorothioate; antiinflammatory;

KW antidiabetic; cytostatic; antipsoriatic; vaccine; gene therapy; cancer;

KW psoriasis; diabetes; enzyme; gene; ds.

XX

OS Homo sapiens.

XX

PN WO200297133-A1.

XX

PD 05-DEC-2002.

XX

PF 21-MAY-2002; 2002WO-US016135.

XX

PR 25-MAY-2001; 2001US-00865866.

XX

PA (ISIS-) ISIS PHARM INC.

XX

PI Bennett CF, Wyatt JR;

XX

DR WPI; 2003-140495/13.

XX

PT New compound that hybridizes with and inhibits the expression of

PT Phospholipase A2, group IIA, useful for preparing a composition for

PT treating or preventing inflammation, cancer, psoriasis or diabetes.

XX

PS Example 15; Page 99-100; 135pp; English.

XX

CC The present invention describes a compound (I) comprising 8-50

CC nucleobases which is targeted to a 5' untranslated region (UTR), coding,

CC 3' UTR or intron region of a nucleic acid molecule encoding phospholipase

CC A2, group IIA (synovial), where the compound specifically hybridises with

CC and inhibits the expression of phospholipase A2, group IIA (synovial).

CC

CC Also described: (1) a composition comprising the compound and a carrier

CC or diluent; (2) a method of inhibiting the expression of phospholipase

CC A2, group IIA in cells or tissues; and (3) a method of treating an animal

CC having a disease or condition associated with phospholipase A2, group IIA

CC (synovial). (1) has antiinflammatory, antidiabetic, cytostatic and

CC antipsoriatic activities, and can be used in vaccines and in gene

CC therapy. The compound (I) can be used for preparing a composition for

CC treating or preventing inflammation, cancer, psoriasis or diabetes. The

CC present sequence represents a human phospholipase A2 group IIA (synovial)

CC nucleotide sequence, which is used in an example from the present

CC invention

XX

XX Sequence 1080 BP; 306 A; 242 C; 303 G; 229 T; 0 U; 0 Other;

SQ

Query Match 73.1%; Score 128; DB 7; Length 1080;

Best Local Similarity 89.9%; Pred. No. 1.5e-33;

Matches 160; Conservative 0; Mismatches 15; Indels 3; Gaps 2;

QY 1 CGCGGCAAAACCTGCTGAATGCTTTGGCATCAGCTACTGACACGTAAG-GGTTTCCCA 59

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

763 CTCGGCAAAACCTGCTGAATGCTTTGGCATCAGCTACTGACACGTAAGGGTTTCCCA 822

QY 60 ATCTCTCAACTCTGTCTCTG--CCAGCTGATGAGGGGAAGAAAGGATTACCTAGGGGTAT 117

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

823 ATCTCTCAACTCTGTCTCTGCGCAGGCTGATGAGGGGAAGAAAGGATTACCTAGGGGTAT 882

QY 118 GGGCGACCAATCCTGAGTCCCACTGACACGCGCCATCCCGAGCTTGTGCCTCAC 175

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

883 GGGCGACCAATCCTGAGTCCCACTGACACGCGCCATCCCGAGCTTGTGCCTCAC 940

RESULT 7

ABL70442/c

ID ABL70442 standard; DNA; 5356 BP.

XX

AC ABL70442;

XX

DT 01-JUL-2002 (first entry)

XX

DE Chemically treated cell signalling DNA sequence complementary to#166.

XX

KW Cell signalling; cytosine methylation; cell signalling disease; cancer;

KW tumour; cytostatic; ds.

XX

OS Unidentified.

XX

PN WO200202807-A2.

XX

PD 10-JAN-2002.

XX

PF 29-JUN-2001; 2001WO-EP007471.

XX

PR 30-JUN-2000; 2000DE-01032529.

XX

PR 01-SEP-2000; 2000DE-01043826.

XX

PA (EPIG-) EPIGENOMICS AG.

XX

PI Olek A, Piepenbrock C, Berlin K;

XX

DR WPI; 2002-154758/20.

XX

PT Nucleic acid, useful for diagnosis and therapy of diseases associated

PT with cell signalling e.g. cancer, comprises chemically modified genomic

PT sequences of genes associated with cell signalling.

XX

PS Claim 1; SEQ ID NO 332; 24pp + Sequence Listing; English.

XX

CC The invention relates to a nucleic acid comprising a sequence of at least

CC 18 bases of a segment of chemically pretreated DNA of genes associated

CC with cell signalling. The activity of the modified sequences of the

CC invention may be described as cytostatic. The object of the invention is

CC to provide the chemically modified DNA of genes associated with cell

CC signalling, as well as oligonucleotides and/or PNA-oligomers for

CC detecting cytosine methylations, as well as a method which is
CC particularly suitable for the diagnosis and/or therapy of genetic and
CC epigenetic parameters of genes associated with cell signalling. The
CC chemically modified DNA provided by the invention is useful for diagnosis
CC and therapy of diseases such as solid tumours and cancer. The sequences
CC given in records ABL70111-ABL70626 represent chemically pre-treated
CC genomic DNA's of genes associated with cell signalling. Note: The
CC sequence data for this patent is not represented in the printed
CC specification, but is based on sequence information supplied by the
CC European Patent Office
XX
SQ Sequence 5356 BP; 1357 A; 60 C; 1167 G; 2772 T; 0 U; 0 Other;

Query Match 63.3%; Score 110.8; DB 6; Length 5356;
Best Local Similarity 78.2%; Pred. No. 2.2e-27;
Matches 133; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 6 CAAAACTGCTGAAATGTGTTTGGCATCAGTACTGACACGTAAGTTCCTCAATCCTC 65
DB 1324 CAAAACTGCTGAAATGTGTTTAAACATCACTACTGACACGTAAGTTCCTCAATCCTC 1265
QY 66 AACTCTGTCTGCTGAGTGGGAGGAAAGGATTAACCTAGGGGTATGGGGACC 125
DB 1264 AACTCTATCTCTACCACTAATAAAAAAATAAAAAATTAACCTAATAAATACGACC 1205
QY 126 AATCTGTAGTCCACCACTGACACGCCCATCCGAGCCTTGCTCTAC 175
DB 1204 AATCTTAATCTCCACCACTAACCACGCCCATCCCACTTATACCTC 1155

RESULT 8
ABK31473/c
ID ABK31473 standard; DNA; 5728 BP.
XX
AC ABK31473;
XX
DT 23-APR-2002 (first entry)
XX
DE Signal transduction associated gene modified complementary DNA #158.

Human; signal transduction associated gene; cytosine methylation state;
KW CpG island; signal transduction associated disease; solid tumour; cancer;
KW antitumour; cytostatic; mutant; ds.
XX

OS Homo sapiens.
OS Synthetic.
XX

WO200200926-A2.
XX

03-JAN-2002.
XX

29-JUN-2001; 2001WO-EP007472.
XX

30-JUN-2000; 2000DE-01032529.
XX

01-SEP-2000; 2000DE-01043826.
XX

(EPIG-) EPIGENOMICS AG.
XX

Olek A, Piepenbrock C, Berlin K;
XX

WPI; 2002-147896/19.
XX

Oligonucleotide for diagnosis and therapy of diseases associated with
PT signal transduction e.g. cancer, comprises chemically modified genomic
PT sequences of genes associated with signal transduction.
XX

Claim 1; SEQ ID NO 316; 24pp; English.
XX

The present invention relates to chemically modified DNA sequences of
CC signal transduction associated genes. The DNA sequences are chemically
CC modified using a solution of bisulphite, hydrogen sulphite or disulphite.
CC Also disclosed are oligonucleotides and/or PNA oligomers for detecting
CC the cytosine methylation state (CpG islands) of these genes, and a method

CC for the diagnosis and/or therapy of genetic and epigenetic parameters of
CC genes associated with signal transduction. The genomic DNA can be
CC obtained from cells or cellular components which contain DNA, e.g. cell
CC lines, biopsies, blood, sputum, stool, urine, cerebral-spinal fluid,
CC tissue embedded in paraffin such as tissue from eyes, intestine, kidney,
CC brain, heart, prostate, lung, breast or liver, histologic object slides,
CC and all their possible combinations. The sequences of the invention are
CC useful for the diagnosis and therapy of diseases associated with signal
CC transduction e.g. solid tumours and cancer. ABK31158-ABK31545 represent
CC chemically pretreated genomic DNA sequences of different genes associated
CC with signal transduction, or their complementary sequences. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC European Patent Office
XX

SQ Sequence 5728 BP; 1462 A; 79 C; 1271 G; 2916 T; 0 U; 0 Other;

Query Match 63.3%; Score 110.8; DB 6; Length 5728;
Best Local Similarity 78.2%; Pred. No. 2.3e-27;
Matches 133; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 6 CAAAACTGCTGAAATGTGTTTGGCATCAGTACTGACACGTAAGTTCCTCAATCCTC 65
DB 969 CAAAACTGCTGAAATGTGTTTAAACATCACTACTAACACGTAAGTTCCTCAATCCTC 910

QY 66 AACTCTGTCTGCTGAGTGGGAGGAAAGGATTAACCTAGGGGTATGGGGACC 125
DB 909 AACTCTATCTCTACCACTAATAAAAAAATAAAAAATTAACCTAATAAATACGACC 850

QY 126 AATCTGTAGTCCACCACTGACACGCCCATCCGAGCCTTGCTCTAC 175
DB 849 AATCTTAATCTCCACCACTAACCACGCCCATCCCACTTATACCTC 800

RESULT 9
AAS46715/c
ID AAS46715 standard; DNA; 6083 BP.
XX
AC AAS46715;
XX
DT 18-DEC-2001 (first entry)
XX
DE Tumour suppressor gene derived chemically modified sequence #438.

Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer;
KW tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
KW cytosine methylation; ds.
XX
OS Homo sapiens.
XX
WO200168912-A2.
XX

20-SEP-2001.
XX

15-MAR-2001; 2001WO-EP002955.
XX

15-MAR-2000; 2000DE-01013847.
XX

06-APR-2000; 2000DE-01019058.
XX

07-APR-2000; 2000DE-01019173.
XX

30-JUN-2000; 2000DE-01032529.
XX

01-SEP-2000; 2000DE-01043826.
XX

(EPIG-) EPIGENOMICS AG.
XX

Olek A, Piepenbrock C, Berlin K;
XX

WPI; 2001-602752/68.
XX

Fragments of chemically modified genes associated with tumor suppressor
PT genes and oncogenes, useful in designing primers and probes for analyzing
PT diseases associated with cytosine methylation state e.g. cancer.
XX
Claim 1; SEQ ID NO 438; 27pp; English.
PS

XX The invention relates to a nucleic acid comprising a sequence of 18
CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
CC bisulphite, of genes associated with tumour suppression and oncogenes
CC having a sequence taken from 536 (actually 533 since numbers 408, 458 and
CC 500 are missing from the sequence listing) sequences (Ss) and sequences
CC complementary to (Ss). The nucleic acid may be a peptide nucleic acid-
CC oligomer (PNA) of at least 9 nucleotides and may form part of a set of
CC probes for detecting the cytosine methylation state and/or single
CC nucleotide polymorphisms and also to be used in an array for analysing
CC diseases associated with CpG dinucleotides e.g. cancers and tumours. The
CC probes can also be used in a method for ascertaining genetic and/or
CC epigenetic parameters for the diagnosis and/or therapy of existing
CC diseases or the predisposition to specific diseases, by analysing
CC cytosine methylations. The parameters may be compared to another set of
CC genetic and/or epigenetic parameters, the differences serving as basis
CC for diagnosis and/or prognosis events which are disadvantageous to
CC patients. The present sequence is one of the 533 genomic sequences
CC derived from tumour suppressor genes and oncogenes. Sequences with even
CC numbered Seq ID numbers are the complementary sequence of the
CC corresponding odd numbered sequence (e.g. ID 2 and ID1, ID 536 and ID
CC 535, except for those whose partner sequence is missing). Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 6083 BP; 1525 A; 83 C; 1367 G; 3108 T; 0 U; 0 Other;

Query Match 63.3%; Score 110.8; DB 4; Length 6083;
Best Local Similarity 78.2%; Pred. No. 2.3e-27;
Matches 133; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 6 CAAGACTGCTGCAATGTTTGGCATCAGTACTGACAGTAAAGTTTCCCAATCTC 65
Db 1324 CAAAACCTACCTAAAATATATTTTAACATCAACTACTAAACGTAATAATTTCCCAATCTC 1265

QY 66 AACTCTGCTCCGACGCTGATGAGGGGAAGGAAGGATTACCTAGGGGTATGGCGACC 125
Db 1264 AACTCTATCTTACCACTAATAAAAAAATAAAAAAATAATTAATTAACGACC 1205

QY 126 AATCTGTAGTCCACCACTGACAGCCATCCCGCCTGCTGCTCAC 175
Db 1204 AATCTTAATCCACCACTAACCAACGCGCATCCCAACCTTATACCTCAC 1155

RESULT 10
ABL70441
ID ABL70441 standard; DNA; 5356 BP.
XX
AC ABL70441;
XX
DT 01-JUL-2002 (first entry)
XX
DE Chemically treated cell signalling DNA sequence#166.
XX
KW Cell signalling; cytosine methylation; cell signalling disease; cancer;
KW tumour; cytostatic; ds.
XX
OS Unidentified.
XX
FN WO200202807-A2.
XX
PD 10-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-EP007471.
XX
PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;

DR WPI; 2002-154758/20.
XX
PT Nucleic acid, useful for diagnosis and therapy of diseases associated
PT with cell signalling e.g. cancer, comprises chemically modified genomic
PT sequences of genes associated with cell signaling.
XX
XX Claim 1; SEQ ID NO 331; 24pp + Sequence Listing; English.
PS
XX The invention relates to a nucleic acid comprising a sequence of at least
CC 18 bases of a segment of chemically pretreated DNA of genes associated
CC with cell signalling. The activity of the modified sequences of the
CC invention may be described as cytostatic. The object of the invention is
CC to provide the chemically modified DNA of genes associated with cell
CC signalling, as well as oligonucleotides and/or PNA-oligoners for
CC detecting cytosine methylations, as well as a method which is
CC particularly suitable for the diagnosis and/or therapy of genetic and
CC epigenetic parameters of genes associated with cell signalling. The
CC chemically modified DNA provided by the invention is useful for diagnoses
CC and therapy of diseases such as solid tumours and cancer. The sequences
CC given in records ABL70411-ABL70626 represent chemically pre-treated
CC genomic DNA's of genes associated with cell signalling. Note: The
CC sequence data for this patent is not represented in the printed
CC specification, but is based on sequence information supplied by the
CC European Patent Office
XX
SQ Sequence 5356 BP; 1476 A; 60 C; 1356 G; 2464 T; 0 U; 0 Other;

Query Match 54.2%; Score 94.8; DB 6; Length 5356;
Best Local Similarity 72.4%; Pred. No. 7e-22;
Matches 123; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 5 GCAGAACTGCTGCAATGTTTGGCATCAGTACTGACAGTAAAGTTTCCCAATCTC 64
Db 4032 GTAAATTTGTTGAAATGTTTGGTATTAGTTATTGATACGTAAGTTTTTAAATTT 4091

QY 65 CAATCTGCTGCTGCCAGCTGATGAGGGGAAGGAAGGATTACCTAGGGGTATGGCGAC 124
Db 4092 TAAATTTGTTTGTAGTTGATGAGGGGAAGGAAGGATTATTAGGGGTATGGCGAT 4151

QY 125 CAATCTGAGTCCACCACTGACCAACGCGCCATCCCAAGCTTGCTCTCA 174
Db 4152 TAAATTTGAGTTTAAATGATTGATACGTTTATTATTTAGTTTGTGTTTA 4201

RESULT 11
ABK31472
ID ABK31472 standard; DNA; 5728 BP.
XX
AC ABK31472;
XX
DT 23-APR-2002 (first entry)
XX
DE Signal transduction associated gene modified DNA #158.
XX
KW Human; signal transduction associated gene; cytosine methylation state;
KW CpG island; signal transduction associated disease; solid tumour; cancer;
KW antitumour; cytostatic; mutant; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
FN WO200200926-A2.
XX
PD 03-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-EP007472.
XX
PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2002-147896/19.
XX
XX Oligonucleotide for diagnosis and therapy of diseases associated with
PT signal transduction e.g. cancer, comprises chemically modified genomic
PT sequences of genes associated with signal transduction.
XX
XX Claim 1; SEQ ID NO 315; 24pp; English.
XX
XX The present invention relates to chemically modified DNA sequences of
CC signal transduction associated genes. The DNA sequences are chemically
CC modified using a solution of bisulphite, hydrogen sulphite or disulphite.
CC Also disclosed are oligonucleotides and/or PNA oligomers for detecting
CC the cytosine methylation state (CpG islands) of these genes, and a method
CC for the diagnosis and/or therapy of genetic and epigenetic parameters of
CC genes associated with signal transduction. The genomic DNA can be
CC obtained from cells or cellular components which contain DNA, e.g. cell
CC lines, biopsies, blood, sputum, stool, urine, cerebral-spinal fluid,
CC tissue embedded in paraffin such as tissue from eyes, intestine, kidney,
CC brain, heart, prostate, lung, breast or liver, histologic object slides,
CC and all their possible combinations. The sequences of the invention are
CC useful for the diagnosis and therapy of diseases associated with signal
CC transduction e.g. solid tumours and cancer. ABK31158-ABK31545 represent
CC chemically pretreated genomic DNA sequences of different genes associated
CC with signal transduction, or their complementary sequences. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC European Patent Office
XX
XX Sequence 5728 BP; 1547 A; 79 C; 1448 G; 2654 T; 0 U; 0 Other;
Query Match 54.2%; Score 94.8; DB 6; Length 5728;
Best Local Similarity 72.4%; Pred. No. 7.1e-22;
Matches 123; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
QY 5 GCAAACTGCTGCTGAAATGCTTTTGGCATCAGCTACTGACACGTAAGGTTTCCCAATCCT 64
Db 4759 GTAAATGTTTGAATGCTTTTGGTATTAGTTATGATACGTAGGTTTAAATTT 4818
QY 65 CAATCTGCTCCTCCAGCTGATGAGGGGAAGGAGGATTACCTAGGGGTATGGCGAC 124
Db 4819 TAATTTGTTTGTAGTTAGTATGAGGGGAAGGAGGATTATTTAGGGGTATGGCGAT 4878
QY 125 CAATCTGAGTCCACCACTGACACGCCCATCCCGAGCTTGCTCA 174
Db 4879 TAATTTGAGTTTAAATTAATTGATTACGTTTATTTTAGTTTGTGTTTA 4928
RESULT 12
ID AAS46714
XX AAS46714 standard; DNA; 6083 BP.
XX AAS46714;
XX
XX 18-DEC-2001 (first entry)
XX Tumour suppressor gene derived chemically modified sequence #437.
XX Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer;
KW tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
KW cytosine methylation; ds.
XX
XX Homo sapiens.
XX
XX WO200168912-A2.
XX
XX 20-SEP-2001.
XX
XX 15-MAR-2001; 2001WO-EP002955.
XX
XX 15-MAR-2000; 2000DE-01013847.
XX 06-APR-2000; 2000DE-01019058.
XX 07-APR-2000; 2000DE-01019173.
PR

PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX
XX (BPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-602752/58.
XX
XX Fragments of chemically modified genes associated with tumor suppressor
PT genes and oncogenes, useful in designing primers and probes for analyzing
PT diseases associated with cytosine methylation state e.g. cancer.
XX
XX Claim 1; SEQ ID NO 437; 27pp; English.
XX
XX The invention relates to a nucleic acid comprising a sequence of 18
CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
CC bisulphite, of genes associated with tumour suppression and oncogenes
CC having a sequence taken from 536 (actually 533 since numbers 408, 458 and
CC 500 are missing from the sequence listing) sequences (SS) and sequences
CC complementary to (SS). The nucleic acid may be a peptide nucleic acid-
CC oligomer (PNA) of at least 9 nucleotides and may form part of a set of
CC probes for detecting the cytosine methylation state and/or single
CC nucleotide polymorphisms and also to be used in an array for analysing
CC diseases associated with CpG dinucleotides e.g. cancers and tumours. The
CC probes can also be used in a method for ascertaining genetic and/or
CC epigenetic parameters for the diagnosis and/or therapy of existing
CC diseases or the predisposition to specific diseases, by analysing
CC cytosine methylations. The parameters may be compared to another set of
CC genetic and/or epigenetic parameters, the differences serving as basis
CC for diagnosis and/or prognosis events which are disadvantageous to
CC patients. The present sequence is one of the 533 genomic sequences
CC derived from tumour suppressor genes and oncogenes. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 6083 BP; 1640 A; 83 C; 1551 G; 2809 T; 0 U; 0 Other;
Query Match 54.2%; Score 94.8; DB 4; Length 6083;
Best Local Similarity 72.4%; Pred. No. 7.3e-22;
Matches 123; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
QY 5 GCAAACTGCTGCTGAAATGCTTTTGGCATCAGCTACTGACACGTAAGGTTTCCCAATCCT 64
Db 4759 GTAAATGTTTGAATGCTTTTGGTATTAGTTATGATACGTAGGTTTAAATTT 4818
QY 65 CAATCTGCTCCTCCAGCTGATGAGGGGAAGGAGGATTACCTAGGGGTATGGCGAC 124
Db 4819 TAATTTGTTTGTAGTTAGTATGAGGGGAAGGAGGATTATTTAGGGGTATGGCGAT 4878
QY 125 CAATCTGAGTCCACCACTGACACGCCCATCCCGAGCTTGCTCA 174
Db 4879 TAATTTGAGTTTAAATTAATTGATTACGTTTATTTTAGTTTGTGTTTA 4928
RESULT 13
ID ABK63588
XX ABK63588 standard; cDNA; 3330 BP.
XX AC ABK63588;
XX
XX 18-JUN-2002 (first entry)
XX
XX Rat sequence differentially expressed in response to a hepatotoxin #1495.
XX Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening;
KW differential expression; centrilobular necrosis; steatosis.
XX
XX Rattus norvegicus.
XX
XX WO200210453-A2.
XX

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OM nucleic - nucleic search, using sw model

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Listing first 45 summaries

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33: em.htg.mus.*

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39: em.htgo.hum.*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	175	100.0	271	6	AX251577	AX251577 Sequence
2	175	100.0	332	6	AX251578	AX251578 Sequence
3	171.4	97.9	1116	6	AX015387	AX015387 Sequence
4	171.4	97.9	1116	6	BD194533	BD194533 Human nuc
C 5	171.4	97.9	1268	6	AX015532	AX015532 Sequence
C 6	171.4	97.9	1268	6	BD194580	BD194580 Human nuc
7	171.4	97.9	8941	9	AX462114	AX462114 Homo sapi
C 8	171.4	97.9	101824	9	AL358253	AL358253 Human DNA
C 9	165	94.3	157470	2	AL360079	AL360079 Homo sapi
10	128	73.1	1080	6	I09231	I09231 Sequence 36
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C 12	110.8	63.3	5356	6	AX348874	AX348874 Sequence
C 13	110.8	63.3	5728	6	AX344469	AX344469 Sequence
C 14	110.8	63.3	6083	6	AX251472	AX251472 Sequence
15	94.8	54.2	5356	6	AX348873	AX348873 Sequence
16	94.8	54.2	5728	6	AX344468	AX344468 Sequence
17	94.8	54.2	6083	6	AX251471	AX251471 Sequence
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19	47	26.9	3330	6	AX401819	AX401819 Sequence
20	47	26.9	3330	10	RNPLA2G	X51529 Rat gene fo
21	47	26.9	150638	2	AC129994	AC129994 Rattus no
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23	47	26.9	282515	2	AC118094	AC118094 Rattus no
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25	44.4	25.4	4438	10	MMU32313	U32313 Mus musculus
C 26	44.4	25.4	41125	10	AC002108	AC002108 Genomic s
C 27	44.4	25.4	186608	10	AL844178	AL844178 Mouse DNA
28	37.6	21.5	497	10	RNPHLP2	X52613 Rat DNA for
29	34.4	19.7	201957	2	AC111113	AC111113 Mus muscu
C 30	33.4	19.1	194218	2	AC121770	AC121770 Mus muscu
C 31	32.4	18.5	1841	9	AK098681	AK098681 Homo sapi
C 32	32.4	18.5	99088	9	AC093401	AC093401 Homo sapi
33	32.4	18.5	119388	9	AC005866	AC005866 Homo sapi
34	32.4	18.5	158608	9	CNS05TDJ	AL358801 Human chr
C 35	32.4	18.5	256870	2	AC096904	AC096904 Rattus no
C 36	32.4	18.5	311677	2	AC118899	AC118899 Rattus no
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C 38	32.2	18.4	150826	9	AL133325	AL133325 Oryza sat
C 39	32.2	18.4	160013	9	AL133325	AL133325 Human DNA
C 40	32.2	18.4	165867	2	AL353609	AL353609 Homo sapi
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42	32.2	18.4	171941	9	AL365274	AL365274 Human DNA
43	32.2	18.4	200395	9	AF274855	AF274855 Homo sapi
44	32	18.3	60945	9	AC079394	AC079394 Homo sapi
C 45	32	18.3	152319	9	AL137001	AL137001 Human DNA

ALIGNMENTS

RESULT 1
AX251577
LOCUS AX251577 Sequence 5 from Patent WO0168845.
DEFINITION AX251577 271 bp DNA linear PAT 05-OCT-2001
ACCESSION AX251577
VERSION AX251577.1 GI:15985000
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Massaad,C., Berenbaum,F., Olivier,J.L., Salvat,C. and Bereziat,G.
TITLE Inflammation-inducible hybrid promoters, vectors containing same
and uses thereof
JOURNAL Patent: WO 0168845-A 5 20-SEP-2001;

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    Location/Qualifiers
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      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
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  Best Local Similarity 100.0%; Pred. No. 1.1e-48;
  Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGGCAAACTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAA 60
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QY 61 TCCTCAACTCTGCTGCGCAGCTGATGAGGGGAAGGAAGGATTACCTAGGGGTATGG 120
Db 61 TCCTCAACTCTGCTGCGCAGCTGATGAGGGGAAGGAAGGATTACCTAGGGGTATGG 120

QY 121 CGACCAATCCTGAGTCCACCACTGACACGCGCCATCCCGAGCTTGTGCTCTCAC 175
Db 121 CGACCAATCCTGAGTCCACCACTGACACGCGCCATCCCGAGCTTGTGCTCTCAC 175

RESULT 2
LOCUS AX251578 332 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 6 from Patent WO0168845.
ACCESSION AX251578
VERSION AX251578.1 GI:15985001
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE
  1
  AUTHORS Massaad,C., Berenbaum,F., Olivier,J.L., Salvat,C. and Bereziat,G.
  TITLE Inflammation-inducible hybrid promoters, vectors containing same
  JOURNAL and uses thereof
  Patent: WO 0168845-A 6 20-SEP-2001;
  Aventis Pharma S.A. (FR)

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    /organism="synthetic construct"
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    /note="promoteur hybride pPRE/PLA2s"

ORIGIN
  Query Match      100.0%; Score 175; DB 6; Length 332;
  Best Local Similarity 100.0%; Pred. No. 1.1e-48;
  Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGGCAAACTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAA 60
Db 62 CGCGGCAAACTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAA 121

QY 61 TCCTCAACTCTGCTGCGCAGCTGATGAGGGGAAGGAAGGATTACCTAGGGGTATGG 120
Db 122 TCCTCAACTCTGCTGCGCAGCTGATGAGGGGAAGGAAGGATTACCTAGGGGTATGG 181

QY 121 CGACCAATCCTGAGTCCACCACTGACACGCGCCATCCCGAGCTTGTGCTCTCAC 175
Db 182 CGACCAATCCTGAGTCCACCACTGACACGCGCCATCCCGAGCTTGTGCTCTCAC 236

RESULT 3
AX015387
LOCUS AX015387 1116 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 53 from Patent WO9951727.
ACCESSION AX015387
VERSION AX015387.1 GI:10041367

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    /note="promoteur hybride pPRE/PLA2s"

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  Best Local Similarity 100.0%; Pred. No. 2e-47;
  Matches 172; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CGCGGCAAACTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAA 62
Db 6 CTGCAAACTGCTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAA 65

QY 63 CTCAACTCTGCTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAA 122
Db 66 CTCAACTCTGCTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAA 125

QY 123 ACCAATCCTGAGTCCACCACTGACACGCGCCATCCCGAGCTTGTGCTCTCAC 175
Db 126 ACCAATCCTGAGTCCACCACTGACACGCGCCATCCCGAGCTTGTGCTCTCAC 178

RESULT 4
LOCUS BD194533 1116 bp DNA linear PAT 17-JUL-2003
DEFINITION Human nucleic acid sequence originating in normal ovarian tissue.
ACCESSION BD194533
VERSION BD194533.1 GI:33004275
KEYWORDS JP 2002510486-A/44.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
  1 (bases 1 to 1116)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Speft,T., Hintzman,B., Shcmitt,A., Pirarski,C., Duhl,E. and
Rosenthal,A.
TITLE Human nucleic acid sequence originating in normal ovarian tissue
JOURNAL Patent: JP 2002510486-A 44 09-APR-2002;
METAGEN GESELLSCHAFT FUER GENOME FORSCHUNG MBH

COMMENT OS Homo sapiens (human)
PS JP 2002510486-A/44
ED 09-APR-2002
EF 31-MAR-1999 JP 2000542440
PR 03-APR-1998 DE 198 16 395.9
PI THOMAS SPEFT,BERND HINTZMAN,ARMIN SHCMITT,CHRISTIAN PIRARSKI,
PI EDGAR DUHL,
PI ANDRE ROSENTHAL
PC C12N15/09,A61K38/00,A61K48/00,A61P35/00,C07K14/47,C07K16/30,
PC C12N1/15,
PC C12N1/19,C12N1/21,C12N5/10,C12Q1/68,G01N33/574,C12N15/00, PC
A61K37/02,
PC C12N5/00
CC Human nucleic acid sequence originating in normal ovarian CC
tissue

PH Key Location/Qualifiers
FT source 1..1116
FT /organism='Homo sapiens (human)'.
FT Location/Qualifiers
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KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
  1
  AUTHORS Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and
  Pilsarsky,C.
  TITLE Human nucleic acid sequences of normal ovary tissue
  JOURNAL Patent: WO 9951727-A 53 14-OCT-1999;
  SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
  BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN
  (DE); PILARSKY CHRISTIAN (DE)
  Location/Qualifiers
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    /db_xref="taxon:9606"

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  Matches 172; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CGCGGCAAACTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAA 62
Db 6 CTGCAAACTGCTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAA 65

QY 63 CTCAACTCTGCTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAA 122
Db 66 CTCAACTCTGCTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAA 125

QY 123 ACCAATCCTGAGTCCACCACTGACACGCGCCATCCCGAGCTTGTGCTCTCAC 175
Db 126 ACCAATCCTGAGTCCACCACTGACACGCGCCATCCCGAGCTTGTGCTCTCAC 178

RESULT 4
LOCUS BD194533 1116 bp DNA linear PAT 17-JUL-2003
DEFINITION Human nucleic acid sequence originating in normal ovarian tissue.
ACCESSION BD194533
VERSION BD194533.1 GI:33004275
KEYWORDS JP 2002510486-A/44.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
  1 (bases 1 to 1116)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Speft,T., Hintzman,B., Shcmitt,A., Pirarski,C., Duhl,E. and
Rosenthal,A.
TITLE Human nucleic acid sequence originating in normal ovarian tissue
JOURNAL Patent: JP 2002510486-A 44 09-APR-2002;
METAGEN GESELLSCHAFT FUER GENOME FORSCHUNG MBH

COMMENT OS Homo sapiens (human)
PS JP 2002510486-A/44
ED 09-APR-2002
EF 31-MAR-1999 JP 2000542440
PR 03-APR-1998 DE 198 16 395.9
PI THOMAS SPEFT,BERND HINTZMAN,ARMIN SHCMITT,CHRISTIAN PIRARSKI,
PI EDGAR DUHL,
PI ANDRE ROSENTHAL
PC C12N15/09,A61K38/00,A61K48/00,A61P35/00,C07K14/47,C07K16/30,
PC C12N1/15,
PC C12N1/19,C12N1/21,C12N5/10,C12Q1/68,G01N33/574,C12N15/00, PC
A61K37/02,
PC C12N5/00
CC Human nucleic acid sequence originating in normal ovarian CC
tissue

PH Key Location/Qualifiers
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FT /organism='Homo sapiens (human)'.
FT Location/Qualifiers
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Matches 172; Conservative 0; Mismatches 1;

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QY 63 CTCAACTCTGCTGCTGCCAGCTGATGAGGGGAAGAAAGGATTACCTAGGGGTATGGGCG 122
Db 66 CTCAACTCTGCTGCTGCCAGCTGATGAGGGGAAGAAAGGATTACCTAGGGGTATGGGCG 125

QY 123 ACCAATCTGAGTCCCAACTGACACGCGCCATCCCGACCTTGTGCTCAC 175
Db 126 ACCAATCTGAGTCCCAACTGACACGCGCCATCCCGACCTTGTGCTCAC 178

RESULT 5
AX015532/c
LOCUS AX015532 1268 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 226 from Patent WO9951727.
ACCESSION AX015532
VERSION AX015532.1 GI:10041414
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
Schmitt, A., Specht, T., Dahl, E., Hinzmann, B., Rosenthal, A. and
Pillarsky, C.
TITLE Human nucleic acid sequences of normal ovary tissue
JOURNAL Patent: WO 9951727-A 226 14-OCT-1999;
SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN
(DE); PILLARSKY CHRISTIAN (DE)
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Matches 172; Conservative 0; Mismatches 1;

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QY 63 CTCAACTCTGCTGCTGCCAGCTGATGAGGGGAAGAAAGGATTACCTAGGGGTATGGGCG 122
Db 1203 CTCAACTCTGCTGCTGCCAGCTGATGAGGGGAAGAAAGGATTACCTAGGGGTATGGGCG 1144

QY 123 ACCAATCTGAGTCCCAACTGACACGCGCCATCCCGACCTTGTGCTCAC 175
Db 1143 ACCAATCTGAGTCCCAACTGACACGCGCCATCCCGACCTTGTGCTCAC 1091

RESULT 6
BD194580/c
LOCUS BD194580 1268 bp DNA linear PAT 17-JUL-2003
DEFINITION Human nucleic acid sequence originating in normal ovarian tissue.
ACCESSION BD194580
VERSION BD194580.1 GI:33004323
KEYWORDS
JP 2002510486-A/91.
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        179
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        450..577
            /rpt_family="L2"
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        845
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            /rpt_type="dispersed"
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Query Match 97.9%; Score 171.4; DB 9; Length 8941;
Best Local Similarity 99.4%; Pred. No. 2.2e-47;
Matches 172; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CGGCAAACTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAATC 62
Db 2530 CTGCAAACTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAATC 2589

QY 63 CTCAACTCTCTCTGCCAGCTGATGAGGGGAAGAAAGGATTAACCTAGGGGTATGGCG 122
Db 2590 CTCAACTCTCTCTGCCAGCTGATGAGGGGAAGAAAGGATTAACCTAGGGGTATGGCG 2649

QY 123 ACCAATCTGAGTCCCAACTGACACGCGCCATCCCGAGCTTGTGCTTCAC 175
Db 2650 ACCAATCTGAGTCCCAACTGACACGCGCCATCCCGAGCTTGTGCTTCAC 2702

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RESULT 8
AL358253/c 101824 bp DNA linear PRI 19-SEP-2002
LOCUS Human DNA sequence from clone RP11-460G22 on chromosome 1, complete
sequence.
ACCESSION AL358253
VERSION AL358253.16 GI:23304623
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
BAGGULEY, C.
Direct Submission
Submitted (19-SEP-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk USA clone requests: clonerequest@sanger.ac.uk
On Sep 23, 2002 this sequence version replaced gi:22797900.
----- Genome Center

```

Center: Wellcome Trust Sanger Institute
 Center code: SC
 Web site: <http://www.sanger.ac.uk>
 Contact: humquerry@sanger.ac.uk

 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e. phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at <http://www.sanger.ac.uk/Projects/C.elegans/wormpep>. This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chrl>. RP11-460G22 is from the library RP11-11.2 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>
 VECTOR: pBACE3.6.

FEATURES

Location/Qualifiers
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ORIGIN

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Best Local Similarity 99.4%; Pred. No. 2.4e-47;
Matches 172; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CGGCAAACTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAATC 62
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QY 63 CTCAACTCTCTCTGCCAGCTGATGAGGGGAAGAAAGGATTAACCTAGGGGTATGGCG 122
Db 73242 CTCAACTCTCTCTGCCAGCTGATGAGGGGAAGAAAGGATTAACCTAGGGGTATGGCG 73183

QY 123 ACCAATCTGAGTCCCAACTGACACGCGCCATCCCGAGCTTGTGCTTCAC 175
Db 73182 ACCAATCTGAGTCCCAACTGACACGCGCCATCCCGAGCTTGTGCTTCAC 73130

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RESULT 9
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LOCUS Homo sapiens chromosome 1 clone RP11-66M4, 22 unordered pieces.
DEFINITION AL360079
ACCESSION AL360079.3 GI:9801103
VERSION HTG; HTGS PHASE1; HTGS_CANCELLED.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
McLay, K.
Direct Submission
Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
JOURNAL

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CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
 On Aug 14, 2000 this sequence version replaced gi:8919533.
 ----- Genome Center
 Center: Sanger Centre
 Center code: SC
 Web site: http://www.sanger.ac.uk
 Contact: humquery@sanger.ac.uk
 ----- Project Information
 Center project name: BA66M4
 ----- Summary Statistics
 Assembly program: XGAP4; version 4.5
 Sequencing vector: plasmid; L08752; 100% of reads
 Chemistry: Dye-terminator ET-amersham; 1% of reads Chemistry:
 Dye-terminator Big Dye; 98% of reads
 Consensus quality: 145607 bases at least Q40
 Consensus quality: 150854 bases at least Q30
 Consensus quality: 153362 bases at least Q20
 Insert size: 155370; sum-of-contigs
 Insert size: 175368; 2.3% error; agarose-fp
 Quality coverage: 3.40x in Q20 bases; sum-of-contigs Quality
 coverage: 3.16x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

* 1 15108: contig of 15108 bp in length
 * 15109 15208: gap of 100 bp
 * 15209 20077: contig of 4869 bp in length
 * 20078 20177: gap of 100 bp
 * 20178 26598: contig of 6421 bp in length
 * 26599 26698: gap of 100 bp
 * 26699 31874: contig of 5176 bp in length
 * 31875 31974: gap of 100 bp
 * 31975 39580: contig of 7606 bp in length
 * 39581 39680: gap of 100 bp
 * 39681 62977: contig of 23297 bp in length
 * 62978 63077: gap of 100 bp
 * 63078 75654: contig of 12577 bp in length
 * 75655 75754: gap of 100 bp
 * 75755 90667: contig of 14913 bp in length
 * 90668 90767: gap of 100 bp
 * 90768 93945: contig of 3178 bp in length
 * 93946 94045: gap of 100 bp
 * 94046 99022: contig of 4977 bp in length
 * 99023 99122: gap of 100 bp
 * 99123 101699: contig of 2577 bp in length
 * 101700 101799: gap of 100 bp
 * 101800 105241: contig of 3442 bp in length
 * 105242 105341: gap of 100 bp
 * 105342 107538: contig of 2197 bp in length
 * 107539 107638: gap of 100 bp
 * 107639 111008: contig of 3370 bp in length
 * 111009 111009: gap of 100 bp
 * 111109 113755: contig of 2647 bp in length
 * 113756 113855: gap of 100 bp
 * 113856 121296: contig of 7441 bp in length
 * 121297 121397: gap of 100 bp
 * 121397 125841: contig of 4445 bp in length
 * 125842 125942: gap of 100 bp
 * 125943 129256: contig of 3315 bp in length
 * 129257 129357: gap of 100 bp
 * 129358 136269: contig of 6913 bp in length
 * 136270 136369: gap of 100 bp
 * 136370 138879: contig of 2510 bp in length
 * 138880 138979: gap of 100 bp
 * 138980 144504: contig of 5525 bp in length
 * 144505 144604: gap of 100 bp

FEATURES
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 136370..138879
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 Db 15386 CTGCAAACTCCCTGAATGTTTGGCAGCTACTGACAGTACCTAGGTTCCCAATC 15327
 QY 63 CTCAACTCTGTCCTGCCAGCTGATGAGGGGAAGAAAGGGATTACCTAGGGGTATGGCG 122
 Db 15326 CTCACCTCTGTCCTGCCAGCTAATGAGGGGAAGAAAGGGATTACCTAGGGGTGTTGGCG 15267
 QY 123 ACCAATCTGATCCACCACTGACCGCCATCCCGCCCTGCTGCTC 175
 Db 15266 ACCATTCTGATCCACCACTGACCGCCATCCCGCCCTGCTGCTC 15214

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Best Local Similarity	89.9%; Pred. No. 1.5e-32;
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Db	763 CTGGCAAAACTGCCTGAATGTGTTTGGCATCAGGCTACTGACGTAGGGTTTCCCA 822
QY	60 ATCCTCAACTCTCTGCTCTG--CCAGCTGATGAGGGGAAGAAAGGGAATTAACCTAGGGGTAT 117
Db	823 ATCCTCAACTCTCTGCTGGCAGGCTGATGAGGGGAAGAAAGGGAATTAACCTAGGGGTAT 882
QY	118 GSGCGACCAATCTGAGTCCACCACTGACACGCCCATCCCGAGCTTTGTGCTCTAC 175
Db	883 GSGCGACCAATCTGAGTCCACCACTGACACGCCCATCCCGAGCTTTGTGCTCTAC 940
RESULT 12	
AX348874/c	
LOCUS	AX348874 5356 bp DNA linear PAT 06-FEB-2002
DEFINITION	Sequence 332 from Patent WO0202807.
ACCESSION	AX348874
VERSION	AX348874.1 GI:18614909
KEYWORDS	synthetic construct
SOURCE	synthetic construct
ORGANISM	artificial sequences.
REFERENCE	1
AUTHORS	Olek, A., Piepenbrock, C. and Berlin, K.
TITLE	Diagnosis of diseases associated with cell signalling
JOURNAL	Patent: WO 0202807-A 332 10-JAN-2002;
FEATURES	Epigenomics AG (DE)
source	Location/Qualifiers
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	/organism="synthetic construct"
	/mol_type="unassigned DNA"
	/db_xref="taxon:32630"
	/note="chemically treated genomic DNA (Homo sapiens)"
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Best Local Similarity	78.3%; Pred. No. 1.3e-26;
Matches 133; Conservative	0; Mismatches 37; Indels 0; Gaps 0;
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Db	1324 CAAACACTCAAATAATATTTTAACATCACTACTACACGTAATAATTCCCAATCCTC 1265
QY	66 AACTCTGTCCTGCAGCTGATGAGGGGAAGAAAGGGAATTAACCTAGGGGTATGGGCGACC 125
Db	1264 AACTCTATCTCTACCACTAATAAAAAAAAAAAAAAAAAAATTAACCTAAAAATATAAACGACC 1205
QY	126 AATCCTCGAGTCCACCACTGACACGCCCATCCCGAGCTTTGTGCTCTAC 175
Db	1204 AATCCTAAATCCCACTAAACCAAGGCAATCCCACTCCCACTTATACCTCTAC 1155
RESULT 13	
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LOCUS	AX344469 5728 bp DNA linear PAT 01-FEB-2002
DEFINITION	Sequence 316 from Patent WO0200926.
ACCESSION	AX344469
VERSION	AX344469.1 GI:18492357
KEYWORDS	synthetic construct
SOURCE	synthetic construct
ORGANISM	artificial sequences.
REFERENCE	1
AUTHORS	Olek, A., Piepenbrock, C. and Berlin, K.
TITLE	Diagnosis of diseases associated with signal transduction
JOURNAL	Patent: WO 0200926-A 316 03-JAN-2002;
FEATURES	Epigenomics AG (DE)
	Location/Qualifiers

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SOURCE
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"

ORIGIN
Query Match      63.3%; Score 110.8; DB 6; Length 5728;
Best Local Similarity 78.2%; Pred. No. 1.3e-26;
Matches 133; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY      6  CAAAACTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAATCCTC 65
DB      969  CAAAACCTACCTAAATATATATTTTAACTCACTAAACGTAATAATTTCCCAATCCTC 910

QY      66  AACTCTGTCCTGCCAGCTGATGAGGGGAAGGAAGGATTACCTAGGGGTATGGCGACC 125
DB      909  AACTCTATCTTACCACCTAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 850

QY      126  AATCTGAGTCCACCACTGACGAGCCATCCCTCCAGCCTTGTGCTCAC 175
DB      849  AATCTCTAAATCCACCACTAAACACCGCCATCCCTCCACCTTATACCTCAC 800

RESULT 14
AX251472/C      AX251472      6083 bp      DNA      linear      PAT 05-OCT-2001
DEFINITION      Sequence 440 from Patent WO0168912.
ACCESSION      AX251472
VERSION      AX251472.1 GI:15984895
KEYWORDS
SOURCE      synthetic construct
ORGANISM      synthetic construct
              artificial sequences.
REFERENCE      1
AUTHORS      Olek,A., Piepenbrock,C. and Berlin,K.
TITLE      Diagnosis of diseases associated with tumor suppressor genes and
              oncogenes
JOURNAL      Patent: WO 0168912-A 440 20-SEP-2001;
Epigenomics AG (DE)
FEATURES      Location/Qualifiers
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              /note="chemically treated genomic DNA (Homo sapiens)"

ORIGIN
Query Match      63.3%; Score 110.8; DB 6; Length 6083;
Best Local Similarity 78.2%; Pred. No. 1.3e-26;
Matches 133; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

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QY      66  AACTCTGTCCTGCCAGCTGATGAGGGGAAGGAAGGATTACCTAGGGGTATGGCGACC 125
DB      1264  AACTCTATCTTACCACCTAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1205

QY      126  AATCTGAGTCCACCACTGACGAGCCATCCCGAGCCTTGTGCTCAC 175
DB      1204  AATCTCTAAATCCACCACTAAACACCGCCATCCCTCCACCTTATACCTCAC 1155

RESULT 15
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LOCUS      AX348873      5356 bp      DNA      linear      PAT 06-FEB-2002
DEFINITION      Sequence 331 from Patent WO0202807.
ACCESSION      AX348873
VERSION      AX348873.1 GI:18614908
KEYWORDS
SOURCE      synthetic construct

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ORGANISM      synthetic construct
              artificial sequences.
REFERENCE      1
AUTHORS      Olek,A., Piepenbrock,C. and Berlin,K.
TITLE      Diagnosis of diseases associated with cell signalling
JOURNAL      Patent: WO 0202807-A 331 10-JAN-2002;
Epigenomics AG (DE)
FEATURES      Location/Qualifiers
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              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="chemically treated genomic DNA (Homo sapiens)"

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Matches 123; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

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DB      4032  GTAAATTTGTTTGAATGTTTGGTATTAGTTATTGATACGTAAGGTTTAAATTTT 4091

QY      65  CAACCTCTGCTCCTGCCAGCTGATGAGGGGAAGGAAGGATTACCTAGGGGTATGGCGAC 124
DB      4092  TAAATTTTGTGTTTGTAGTTGATGAGGGGAAGGAAGGATTATTAGGGGTATGGCGAT 4151

QY      125  CAATCTGAGTCCACCACTGACCAACGCCCATCCCGACCTTGTGCTCA 174
DB      4152  TAAATTTGAGTTTATTAAATGATTACGTTTATTTTAGTTTGTGTTTA 4201

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Job time : 3557 secs

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GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 08:16:17 ; Search time 148,438 Seconds
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Title: US-09-808-388-7
Perfect score: 944
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	169.6	18.0	7664	4	US-08-994-689C-10
4	144	15.3	8083	3	US-09-383-630-4
5	144	15.3	8083	3	US-09-383-630-5
6	114.2	12.1	246	4	US-09-857-063-16
7	114.2	12.1	282	4	US-09-857-063-5
8	113	12.0	244	4	US-09-857-063-14
9	113	12.0	283	4	US-09-857-063-3
10	112.8	11.9	246	4	US-09-857-063-15
11	112.8	11.9	283	4	US-09-857-063-4
12	112.6	11.9	241	4	US-09-857-063-24
13	112.6	11.9	277	4	US-09-857-063-12
14	111.4	11.8	247	4	US-09-857-063-17
15	111.4	11.8	256	4	US-09-857-063-18
16	111.4	11.8	256	4	US-09-857-063-19
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24	104.4	11.1	34303	3	US-09-244-752-4
25	104.4	11.1	34303	3	US-09-245-497-4
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34 104.4 11.1 35935 3 US-08-373-452-43 Sequence 43, Appli
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36 104.4 11.1 35935 3 US-09-244-752-1 Sequence 1, Appli
37 104.4 11.1 35935 3 US-09-245-497-1 Sequence 1, Appli
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41 .98 10.4 343 5 PCT-US93-08067-1 Sequence 1, Appli
42 86.8 9.2 36519 3 US-08-923-137-2 Sequence 2, Appli
43 78.8 8.3 266 5 PCT-US93-08067-2 Sequence 2, Appli
44 69.6 7.4 35524 3 US-08-923-137-1 Sequence 1, Appli
45 64.8 6.9 35081 2 US-08-752-760A-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-994-689C-3
; Sequence 3, Application US/08994689C
; Patent No. 6613958
; GENERAL INFORMATION:
; APPLICANT: Neuhold, Lisa
; APPLICANT: Killar, Loran
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR
; TITLE OF INVENTION: DEGENERATIVE DISEASES OF CARTILAGE
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/994,689C
; FILING DATE: 1997-12-19
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 0630/0D532
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3479 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-994-689C-3

Query Match 18.0%; Score 169.6; DB 4; Length 3479;
Best Local Similarity 80.8%; Pred. No. 7.5e-35;
Matches 210; Conservative 0; Mismatches 49; Indels 1; Gaps 1;

QY 410 CCGTGCCCGCCGCGCCACCTTCATCGATTCGGATTGGCAGCGATGCTCCAGA 469

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Qy 530 GCTCTGTATGCGCTTGAGAAAGCCCATTCATGAGAGCAAGGCCAGTGGGT-CCCC 588
Db 1107 GCTCTGTATGCGCTTGAGAAAGCCCATTCATGAGAGCAAGGCCAGTGGGTCCCC 1166
Qy 589 AACTCCCGACCCCTCTCCACAAATGACAGCCTCCCGCCCTCATCCCCCCCCCAC 648
Db 1167 GACTCCCGACCCCTCTCCACAAATATATCCCCCTCTCTGTGCGCCCTGCGGCCAC 1226
Qy 649 CCCCCGTCGCCCTGCGGC 668
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RESULT 2

US-08-994-689C-9
; Sequence 9, Application US/08994689C
; Patent No. 6613958

; GENERAL INFORMATION:
; APPLICANT: Neuhold, Lisa
; APPLICANT: Killar, Loran
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR
; TITLE OF INVENTION: DEGENERATIVE DISEASES OF CARTILAGE
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/994,689C
FILING DATE: 1997-12-19
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 0630/0D532
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
TELEX: 236687

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 5276 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-994-689C-9

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Best Local Similarity 80.8%; Pred. No. 8.5e-35;
Matches 210; Conservative 0; Mismatches 49; Indels 1; Gaps 1;

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RESULT 3

US-08-994-689C-10
; Sequence 10, Application US/08994689C
; Patent No. 6613958

; GENERAL INFORMATION:
; APPLICANT: Neuhold, Lisa
; APPLICANT: Killar, Loran
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR
; TITLE OF INVENTION: DEGENERATIVE DISEASES OF CARTILAGE
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/994,689C
FILING DATE: 1997-12-19
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 0630/0D532
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
TELEX: 236687

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 7664 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-994-689C-10

Query Match 18.0%; Score 169.6; DB 4; Length 7664;

Best Local Similarity 80.8%; Pred. No. 9.5e-35;
Matches 210; Conservative 0; Mismatches 49; Indels 1; Gaps 1;

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Db 1048 TGGCTGAAACCTCGCCGTAATTTATTTAACTGTTCTCTGGAGAGCTGTGAATCGG 1107
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Db 1108 GCTCTGATGCGCTCGAGAAAGCCCATTCATGAGAGGCAAGCCAGTGGGTCCCC 1167
QY 589 AACTCCCGGACCCCTCTCCCAATGACAGGCTCCCGCCCTCATCCCGCCCGCAC 648
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Db 1228 CTCGCGGCTCGGCGCCGC 1247
RESULT 4
US-09-383-630-4
; Sequence 4, Application US/09383630A
; Patent No. 6265632
; GENERAL INFORMATION:
; APPLICANT: Avner Yayon et al.
; TITLE OF INVENTION: ANIMAL MODEL FOR FIBROBLAST GROWTH
; FACTOR RECEPTOR ASSOCIATED
; CHONDRODYSPLASIA
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
; STREET: 2001 Jefferson Davis Highway, Suite 207
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
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; SOFTWARE: Word for Windows version 2.0 converted
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; FILING DATE: 26-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedman, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 1402/2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-5625553
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
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Best Local Similarity 96.7%; Pred. No. 4.6e-28;
Matches 147; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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QY 792 GTCATACTTATCTGTCCTCTTTTTCACAGCTCGCGGTTCAGGACAAACTCTTCGCG 851

Db 4927 GTCATACTTATCTGTCCTCTTTTTCACAGCTCGCGGTTCAGGACAAACTCTTCGCG 4986
QY 852 GTCTTTCCAGTGGGATCGACGGTATCGATAA 883
Db 4987 GTCTTTCCAGTGGGATCGACGGTATCGATCA 5018
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US-09-383-630-5
; Sequence 5, Application US/09383630A
; Patent No. 6265632
; GENERAL INFORMATION:
; APPLICANT: Avner Yayon et al.
; TITLE OF INVENTION: ANIMAL MODEL FOR FIBROBLAST GROWTH
; FACTOR RECEPTOR ASSOCIATED
; CHONDRODYSPLASIA
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
; STREET: 2001 Jefferson Davis Highway, Suite 207
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22202
; COMPUTER READABLE FORM:
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; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; Windows version 3.11
; SOFTWARE: Word for Windows version 2.0 converted
; to an ASCII file
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; FILING DATE: 26-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedman, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 1402/2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-5625553
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8083
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-383-630-5
Query Match 15.3%; Score 144; DB 3; Length 8083;
Best Local Similarity 96.7%; Pred. No. 4.6e-28;
Matches 147; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 732 TAGTGGATCCCCGGCTGCAGATCTGTAGGCGCAGTAGTCCAGGGTTTCTTGATGAT 791
Db 4867 TAGTGGATCCCCGGCTGCAGATCCCCCGGCGCAGTAGTCCAGGGTTTCTTGATGAT 4926
QY 792 GTCATACTTATCTGTCCTCTTTTTCACAGCTCGCGGTTCAGGACAAACTCTTCGCG 851
Db 4927 GTCATACTTATCTGTCCTCTTTTTCACAGCTCGCGGTTCAGGACAAACTCTTCGCG 4986
QY 852 GTCTTTCCAGTGGGATCGACGGTATCGATAA 883
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RESULT 6
US-09-857-063-16
; Sequence 16, Application US/09857063
; Patent No. 6579681
; GENERAL INFORMATION:
; APPLICANT: Huls, Christoph
; APPLICANT: Bauer, Bettina
; APPLICANT: Simandi, Claus
; APPLICANT: Luhrmann, Reinhard
; APPLICANT: Achsel, Tilmann
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: Test System for Detecting a Splicing Reaction and Use Thereof
; FILE REFERENCE: 199at.01.us (8602*34)
; CURRENT APPLICATION NUMBER: US/09/857,063
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: PCT/EP00/01595
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: DE 199 09 156.0
; PRIOR FILING DATE: 1999-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 246
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pre-mRNA
US-09-857-063-16

Query Match      12.1%; Score 114.2; DB 4; Length 246;
Best Local Similarity 87.4%; Pred. No. 9.4e-21;
Matches 125; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 727 AGCTTAGTGATGATCCCGGGGTGCAGATCTGTAGGGCGCAGTAGTCCAGGGTTTCCTTG 786
Db 103 AGCACTTCTGCGCCCAAGCTTGTCAGCTGTAGGGCGCAGTAGTCCAGGGTTTCCTTG 162
QY 787 ATGATGTCACTATCTCTGTCCTTTTTCACAGCTCGGGTTGAGGACAACTCT 846
Db 163 ATGATGTCACTATCTCTGTCCTTTTTCACAGCTCGGGTTGAGGACAACTCT 222
QY 847 TCGCGGTCTTCCAGTGGGGATC 869
Db 223 TCGCGGTCTTCCAGTGGGGATC 245

RESULT 7
US-09-857-063-5
; Sequence 5, Application US/09857063
; Patent No. 6579681
; GENERAL INFORMATION:
; APPLICANT: Huls, Christoph
; APPLICANT: Bauer, Bettina
; APPLICANT: Simandi, Claus
; APPLICANT: Luhrmann, Reinhard
; APPLICANT: Achsel, Tilmann
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: Test System for Detecting a Splicing Reaction and Use Thereof
; FILE REFERENCE: 199at.01.us (8602*34)
; CURRENT APPLICATION NUMBER: US/09/857,063
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: PCT/EP00/01595
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: DE 199 09 156.0
; PRIOR FILING DATE: 1999-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 282
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pre-mRNA
US-09-857-063-5

Query Match      12.1%; Score 114.2; DB 4; Length 246;
Best Local Similarity 87.4%; Pred. No. 9.4e-21;
Matches 125; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 727 AGCTTAGTGATGATCCCGGGGTGCAGATCTGTAGGGCGCAGTAGTCCAGGGTTTCCTTG 786
Db 103 AGCACTTCTGCGCCCAAGCTTGTCAGCTGTAGGGCGCAGTAGTCCAGGGTTTCCTTG 162
QY 787 ATGATGTCACTATCTCTGTCCTTTTTCACAGCTCGGGTTGAGGACAACTCT 846
Db 163 ATGATGTCACTATCTCTGTCCTTTTTCACAGCTCGGGTTGAGGACAACTCT 222
QY 847 TCGCGGTCTTCCAGTGGGGATC 869
Db 223 TCGCGGTCTTCCAGTGGGGATC 245
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US-09-857-063-5

Query Match      12.1%; Score 114.2; DB 4; Length 282;
Best Local Similarity 87.4%; Pred. No. 9.7e-21;
Matches 125; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 727 AGCTTAGTGATGATCCCGGGGTGCAGATCTGTAGGGCGCAGTAGTCCAGGGTTTCCTTG 786
Db 139 AGCACTTCTGCGCCCAAGCTTGTCAGCTGTAGGGCGCAGTAGTCCAGGGTTTCCTTG 198
QY 787 ATGATGTCACTATCTCTGTCCTTTTTCACAGCTCGGGTTGAGGACAACTCT 846
Db 139 ATGATGTCACTATCTCTGTCCTTTTTCACAGCTCGGGTTGAGGACAACTCT 258
QY 847 TCGCGGTCTTCCAGTGGGGATC 869
Db 259 TCGCGGTCTTCCAGTGGGGATC 281

RESULT 8
US-09-857-063-14
; Sequence 14, Application US/09857063
; Patent No. 6579681
; GENERAL INFORMATION:
; APPLICANT: Huls, Christoph
; APPLICANT: Bauer, Bettina
; APPLICANT: Simandi, Claus
; APPLICANT: Luhrmann, Reinhard
; APPLICANT: Achsel, Tilmann
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: Test System for Detecting a Splicing Reaction and Use Thereof
; FILE REFERENCE: 199at.01.us (8602*34)
; CURRENT APPLICATION NUMBER: US/09/857,063
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: PCT/EP00/01595
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: DE 199 09 156.0
; PRIOR FILING DATE: 1999-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pre-mRNA
US-09-857-063-14

Query Match      12.0%; Score 113; DB 4; Length 244;
Best Local Similarity 95.9%; Pred. No. 1.9e-20;
Matches 116; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 85 TCTAGGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCTACTTATCTCTGTCCTTTT 144
QY 817 TTCCACAGCTCGGGTTGAGGACAACTCTTCGCGGTCTTCCAGTGGGGATCCAGCGTA 876
Db 145 TTCCACAGCTCGGGTTGAGGACAACTCTTCGCGGTCTTCCAGTGGGGATCCAGCGTA 204
QY 877 T 877
Db 205 T 205

RESULT 9
US-09-857-063-3
; Sequence 3, Application US/09857063
; Patent No. 6579681
; GENERAL INFORMATION:
; APPLICANT: Huls, Christoph
; APPLICANT: Bauer, Bettina
; APPLICANT: Simandi, Claus
; OTHER INFORMATION: pre-mRNA
US-09-857-063-3
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pre-mRNA
US-09-857-063-24

Query Match      11.9%; Score 112.6; DB 4; Length 241;
Best Local Similarity 96.6%; Pred. No. 2.4e-20;
Matches 115; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 757 TGTAGGCGCAGTAGTCCAGGGTTTCCTTGATGATGCATATCTATCTGTCCTCCCTTTT 816
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QY 817 TTCCACAGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTCCAGTGGGATCGACGGT 875
DB 148 TTCCACAGCTCGCGGTTGAGGACAACTCTTCGCGGTCTTTCCAGTGGGATCGGGAT 206

RESULT 13
US-09-857-063-12
; Sequence 12, Application US/09857063
; Patent No. 6579681
; GENERAL INFORMATION:
; APPLICANT: Huls, Christoph
; APPLICANT: Bauer, Bettina
; APPLICANT: Simandi, Claus
; APPLICANT: Luhrmann, Reinhard
; APPLICANT: Achsel, Tilmann
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: Test System for Detecting a Splicing Reaction and Use Thereof
; FILE REFERENCE: 199at.01.us (8602*34)
; CURRENT APPLICATION NUMBER: US/09/857,063
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: PCT/EP00/01595
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: DE 199 09 156.0
; PRIOR FILING DATE: 1999-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 277
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pre-mRNA
US-09-857-063-12

Query Match      11.9%; Score 112.6; DB 4; Length 277;
Best Local Similarity 96.6%; Pred. No. 2.5e-20;
Matches 115; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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DB 124 TCTAGGGCGCAGTAGTCCAGGGTTTCCTTGATGATGCATATCTATCTGTCCTCCCTTTT 183

QY 817 TTCCACAGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTCCAGTGGGATCGACGGT 875
DB 184 TTCCACAGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTCCAGTGGGATCGGGAT 242

RESULT 14
US-09-857-063-17
; Sequence 17, Application US/09857063
; Patent No. 6579681
; GENERAL INFORMATION:
; APPLICANT: Huls, Christoph
; APPLICANT: Bauer, Bettina
; APPLICANT: Simandi, Claus
; APPLICANT: Luhrmann, Reinhard
; APPLICANT: Achsel, Tilmann
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: Test System for Detecting a Splicing Reaction and Use Thereof
; FILE REFERENCE: 199at.01.us (8602*34)
; CURRENT APPLICATION NUMBER: US/09/857,063
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: PCT/EP00/01595
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: DE 199 09 156.0
; PRIOR FILING DATE: 1999-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pre-mRNA
US-09-857-063-17

Query Match      11.8%; Score 111.4; DB 4; Length 256;
Best Local Similarity 99.1%; Pred. No. 5.1e-20;
Matches 112; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 757 TGTAGGCGCAGTAGTCCAGGGTTTCCTTGATGATGCATATCTATCTGTCCTCCCTTTT 816
DB 143 TCTAGGGCGCAGTAGTCCAGGGTTTCCTTGATGATGCATATCTATCTGTCCTCCCTTTT 202

QY 817 TTCCACAGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTCCAGTGGGATC 869
DB 203 TTCCACAGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTCCAGTGGGATC 255

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Job time : 150.438 secs
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OM nucleic - nucleic search, using sw model

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(without alignments)
5187.326 Million cell updates/sec

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Perfect score: 944
Sequence: 1 tgcgcgctcgctgagcc.....cgtcgtgactgggaaaccc 944

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 6608766

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/US06_PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	169.6	18.0	3479	15	Sequence 7, Appli
3	169.6	18.0	5276	15	Sequence 3, Appli
4	169.6	18.0	7664	15	Sequence 9, Appli
5	122.4	13.0	5887	15	Sequence 10, Appl
6	104.4	11.1	1240	9	Sequence 73, Appl
7	104.4	11.1	1240	9	Sequence 28, Appl
8	104.4	11.1	1240	9	Sequence 32, Appl
9	104.4	11.1	7231	10	Sequence 42, Appl
10	104.4	11.1	7231	10	Sequence 64, Appl
11	104.4	11.1	7960	9	Sequence 38, Appl
12	104.4	11.1	7960	9	Sequence 44, Appl
13	104.4	11.1	7989	9	Sequence 30, Appl
14	104.4	11.1	7989	10	Sequence 33, Appl
					Sequence 47, Appl
					Sequence 29, Appl

15	104.4	11.1	8383	10	US-09-482-682-43	Sequence 43, Appl
16	104.4	11.1	8484	10	US-09-482-682-65	Sequence 65, Appl
17	104.4	11.1	10491	15	US-10-359-050-18	Sequence 18, Appl
18	104.4	11.1	11784	15	US-10-359-050-20	Sequence 20, Appl
19	104.4	11.1	11784	16	US-10-014-099F-106	Sequence 106, App
20	104.4	11.1	12538	15	US-10-359-050-12	Sequence 12, Appl
21	104.4	11.1	12645	15	US-10-359-050-13	Sequence 13, Appl
22	104.4	11.1	30365	13	US-10-384-136-4	Sequence 4, Appl
23	104.4	11.1	31183	17	US-10-431-598-19	Sequence 19, Appl
24	104.4	11.1	31672	13	US-10-384-136-3	Sequence 3, Appl
25	104.4	11.1	31880	16	US-10-427-717-507	Sequence 3, Appl
26	104.4	11.1	32480	9	US-09-847-101B-23	Sequence 507, App
27	104.4	11.1	32480	10	US-09-482-682-27	Sequence 23, Appl
28	104.4	11.1	32798	15	US-10-424-638-1	Sequence 27, Appl
29	104.4	11.1	33622	16	US-10-403-337-44	Sequence 1, Appl
30	104.4	11.1	33622	16	US-10-351-890-44	Sequence 44, Appl
31	104.4	11.1	33855	16	US-10-383-846-5	Sequence 44, Appl
32	104.4	11.1	34427	10	US-09-111-911-5	Sequence 5, Appl
33	104.4	11.1	34555	15	US-10-117-982-479	Sequence 5, Appl
34	104.4	11.1	34555	16	US-10-313-986-479	Sequence 5, Appl
35	104.4	11.1	34573	16	US-10-313-986-479	Sequence 479, App
36	104.4	11.1	34616	13	US-10-383-846-1	Sequence 479, App
37	104.4	11.1	35211	16	US-10-384-136-2	Sequence 1, Appl
38	104.4	11.1	35211	16	US-10-403-337-43	Sequence 2, Appl
39	104.4	11.1	35408	15	US-10-351-890-43	Sequence 43, Appl
40	104.4	11.1	35871	9	US-10-155-649-3	Sequence 43, Appl
41	104.4	11.1	35935	9	US-09-956-335-2	Sequence 3, Appl
42	104.4	11.1	35935	9	US-09-725-720-43	Sequence 2, Appl
43	104.4	11.1	35935	9	US-09-782-378A-4	Sequence 4, Appl
44	104.4	11.1	35935	9	US-09-782-378A-5	Sequence 5, Appl
45	104.4	11.1	35935	10	US-09-739-007-43	Sequence 43, Appl
	104.4	11.1	35935	17	US-10-264-839-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-808-388-7
; Sequence 7, Application US/09808388
; Patent No. US20020081719A1
; GENERAL INFORMATION:
; APPLICANT: Massaad, Charbel
; APPLICANT: Berenbaum, Francis
; APPLICANT: Olivier, Jean-Luc
; APPLICANT: Salvat, Colette
; APPLICANT: Berezat, Gilbert
; TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising them
; TITLE OF INVENTION: their uses
; FILE REFERENCE: ST00010
; CURRENT APPLICATION NUMBER: US/09/808,388
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: FR/00/03262
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/196,959
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 7
; LENGTH: 944
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence conferring specificity of expression
US-09-808-388-7

Query Match 100.0%; Score 944; DB 9; Length 944;
Best Local Similarity 100.0%; Pred. No. 4.4e-272;
Matches 944; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCTGGCTCGGGTACGCCCTGATCCGCTCGGGCTCCCAAGTCGTGCTGCTGA 60
Db 1 TCCTGGCTCGGGTACGCCCTGATCCGCTCGGGCTCCCAAGTCGTGCTGCTGA 60

61 CGTGTCTATCGCCGCGTCTCTAGGTGTAGGCGCAGGATGCGCGTAAAGTCCGCCCG 120
Db
61 CGTGTCTATCGCCGCGTCTCTAGGTGTAGGCGCAGGATGCGCGTAAAGTCCGCCCG 120
Qy
121 CCCCTGCTACTCCCTGACTGTGACCCCTTTCTCTACTCTCCCTCCCAAGTACTAG 180
Db
121 CCCCTGCTACTCCCTGACTGTGACCCCTTTCTCTACTCTCCCTCCCAAGTACTAG 180
Qy
181 GATCCCCCTAGAGCTTGAGATCTGGGATTTGGCAGCGATGGCTTCCAGATGGCTGAAAC 240
Db
181 GATCCCCCTAGAGCTTGAGATCTGGGATTTGGCAGCGATGGCTTCCAGATGGCTGAAAC 240
Qy
241 CCTGCCCTATTTATTTAAACTGGTTCTCTGTGAGAGCTGTGAATCGGCTCTGTATGC 300
Db
241 CCTGCCCTATTTATTTAAACTGGTTCTCTGTGAGAGCTGTGAATCGGCTCTGTATGC 300
Qy
301 GCTTGAGAAAGCCCATTCATGAGAGCAAGGCCAGTGGTGGTCCCACTCCCGGACC 360
Db
301 GCTTGAGAAAGCCCATTCATGAGAGCAAGGCCAGTGGTGGTCCCACTCCCGGACC 360
Qy
361 CCCCTCTCCCAATGCAAGCAGCTCCCGCCCTCATCCCGCCCTCATCCCGCCCTGCGCGC 420
Db
361 CCCCTCTCCCAATGCAAGCAGCTCCCGCCCTCATCCCGCCCTCATCCCGCCCTGCGCGC 420
Qy
421 CTGCGCCGACCTTCAGATCGATCTGGGATTTGGCAGCGATGGCTTCCAGATGGCTGAAAC 480
Db
421 CTGCGCCGACCTTCAGATCGATCTGGGATTTGGCAGCGATGGCTTCCAGATGGCTGAAAC 480
Qy
481 CCTGCCCTATTTATTTAAACTGGTTCTCTGTGAGAGCTGTGAATCGGCTCTGTATGC 540
Db
481 CCTGCCCTATTTATTTAAACTGGTTCTCTGTGAGAGCTGTGAATCGGCTCTGTATGC 540
Qy
541 GCTTGAGAAAGCCCATTCATGAGAGCAAGGCCAGTGGTGGTCCCACTCCCGGACC 600
Db
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Qy
601 CCCCTCTCCCAATGCAAGCAGCTCCCGCCCTCATCCCGCCCTCATCCCGCCCTGCGCGC 660
Db
601 CCCCTCTCCCAATGCAAGCAGCTCCCGCCCTCATCCCGCCCTCATCCCGCCCTGCGCGC 660
Qy
661 CTGCGCCGACCTTCAGATCGATCTGGGATTTGGCAGCGATGGCTTCCAGATGGCTGAAAC 720
Db
661 CTGCGCCGACCTTCAGATCGATCTGGGATTTGGCAGCGATGGCTTCCAGATGGCTGAAAC 720
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721 AAGCCAAAGCTCTAGTGTGATCCCCCGGCTGCAGATCTGTAGGGCGAGTGTCCAGGTT 780
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781 TCCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
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781 TCCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
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841 AACTCTTCGCGGCTTTTCCAGTGGGATCGACGATCGATGATGATGATGATGATGATGATGAT 900
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841 AACTCTTCGCGGCTTTTCCAGTGGGATCGACGATCGATGATGATGATGATGATGATGATGAT 900
Qy
901 ATGCGGATCCCGCTGCTTTTACAACTGCTGATGAGGAAACCC 944
Db
901 ATGCGGATCCCGCTGCTTTTACAACTGCTGATGAGGAAACCC 944

RESULT 2
US-10-375-884-3
; Sequence 3, Application US/10375884
; Publication No. US20030159165A1
; GENERAL INFORMATION:
; APPLICANT: NEUHOLD, Lisa A.
; APPLICANT: KILLAR, Loran Marie
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR DEGENERATIVE DISEASES OF CARTILAGE
; FILE REFERENCE: 0630/1D532US2
; CURRENT APPLICATION NUMBER: US/10/375,884
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 08/994,689

PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 3479
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: type II collagen promoter
US-10-375-884-3

Query Match 18.0%; Score 169.6; DB 15; Length 3479;
Best Local Similarity 80.8%; Pred. No. 3.7e-40;
Matches 210; Conservative 0; Mismatches 49; Indels 1; Gaps 1;

Qy 410 CCCGTGCCGCTGCCGCCACCTTCAGATCGATCTGGGATTTGGCAGCGATGGCTTCCAGA 469
Db 988 CCTCAGTCTCTTTGTGAGGCTTGTTCGTTGAGGATTTGGCAGCGATGGCTTCCAGA 1047
Qy 470 TGGGCTGAAACCCCTGCCCGCTATTTAAACTGGTTCCTCTGTGAGAGCTGTGAATCGG 529
Db 1048 TGGGCTGAAACCCCTGCCCGCTATTTAAACTGGTTCCTCTGTGAGAGCTGTGAATCGG 1107
Qy 530 GCTCTGTATGGCTTTGAGAAAGCCCATTCATGAGAGCAAGGCCAGTGGTGGTCCCGCC 588
Db 1167 GACTCTGATGCTGCTGAGAAAGCCCATTCATGAGAGCAAGGCCAGTGGTGGTCCCGCC 1226
Qy 649 CCCCGTGGCCGCTGCCGC 668
Db 1227 CTCCTGGGCTCCGGCCCCGC 1246

RESULT 3
US-10-375-884-9
; Sequence 9, Application US/10375884
; Publication No. US20030159165A1
; GENERAL INFORMATION:
; APPLICANT: NEUHOLD, Lisa A.
; APPLICANT: KILLAR, Loran Marie
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR DEGENERATIVE DISEASES OF CARTILAGE
; FILE REFERENCE: 0630/1D532US2
; CURRENT APPLICATION NUMBER: US/10/375,884
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 08/994,689
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 5276
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: transgene
US-10-375-884-9

Query Match 18.0%; Score 169.6; DB 15; Length 5276;
Best Local Similarity 80.8%; Pred. No. 3.7e-40;
Matches 210; Conservative 0; Mismatches 49; Indels 1; Gaps 1;

Qy 410 CCCGTGCCGCTGCCGCCACCTTCAGATCGATCTGGGATTTGGCAGCGATGGCTTCCAGA 469
Db 988 CCTCAGTCTCTTTGTGAGGCTTGTTCGTTGAGGATTTGGCAGCGATGGCTTCCAGA 1047
Qy 470 TGGGCTGAAACCCCTGCCCGCTATTTAAACTGGTTCCTCTGTGAGAGCTGTGAATCGG 529
Db 1048 TGGGCTGAAACCCCTGCCCGCTATTTAAACTGGTTCCTCTGTGAGAGCTGTGAATCGG 1107
Qy 530 GCTCTGTATGGCTTTGAGAAAGCCCATTCATGAGAGCAAGGCCAGTGGTGGTCCCGCC 588
Db 1167 GACTCTGATGCTGCTGAGAAAGCCCATTCATGAGAGCAAGGCCAGTGGTGGTCCCGCC 1226
Qy 649 CCCCGTGGCCGCTGCCGC 668
Db 1227 CTCCTGGGCTCCGGCCCCGC 1246

Db 1108 GCTGTGTATGCGCTCGAGAAAAGCCCATTCATGAGAGGAAAGCCAGTGGGTCCCGCC 1167
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Db 1168 GACTCCCGAGCCCTCTCCACATATATCCCGCCCTCCCTGTGCGCGCTCGCGCCAC 1227
QY 649 CCGCGTCCCGCGCTCGCGC 668
Db 1228 CTCGGGCTCGCGCCCGC 1247

RESULT 4

US-10-375-884-10
; Sequence 10, Application US/10375884
; Publication No. US20030159165A1
; GENERAL INFORMATION:
; APPLICANT: NEUHOLD, Lisa A.
; APPLICANT: KILLAR, Loran Marie
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR DEGENERATIVE DISEASES OF CARTILAGE
; FILE REFERENCE: 0630/1D532US2
; CURRENT APPLICATION NUMBER: US/10/375,884
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 2003-02-27
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 21
; SEQ ID NO 10
; LENGTH: 7664
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: transgene
US-10-375-884-10

Query Match 18.0%; Score 169.6; DB 15; Length 7664;
Best Local Similarity 80.8%; Pred. No. 4.1e-40;
Matches 210; Conservative 0; Mismatches 49; Indels 1; Gaps 1;

QY 410 CCGTGCCCGCTCGCGCCACCTTCAGATCGATCTGGATGGGAGGATGGCGATGGCTTCGAGA 469
Db 988 CTCAGTCTCTTGTGAGGCTTGTGCTTGGAGGATGGCAGGATGGCTTCGAGA 1047
QY 470 TGGCTGAACCCCTGCCGCTATTATTAACCTGTTCTCGTGAGAGCTGTGAATCGG 529
Db 1048 TGGCTGAACCCCTGCCGCTATTATTAACCTGTTCTCGTGAGAGCTGTGAATCGG 1107
QY 530 GCTCTGTATGCGCTTGAGAAAGCCCATTCATGAGAGGCAAGCCCGAGTGGGT-CCCC 588
Db 1108 GCTCTGTATGCGCTCGAGAAAGCCCATTCATGAGAGGCAAGCCCGAGTGGGTCCCC 1167
QY 589 AACTCCCGAGCCCTCTCCCAATGACAGCTCCCGCCCTCATCTCCCGCCCGCCAC 648
Db 1168 GACTCCCGAGCCCTCTCCCAATATATATATATATATATATATATATATATATATAT 1227
QY 649 CCGCGTCCCGCTCGCGC 668
Db 1228 CTCGGGCTCGCGCCCGC 1247

RESULT 5

US-10-277-161-73
; Sequence 73, Application US/10277161
; Publication No. US20030194696A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; APPLICANT: Smith, Ernest S.
; TITLE OF INVENTION: Methods of Producing a Library and Methods of Selecting Polynucle
; FILE REFERENCE: 1821.0050006
; CURRENT APPLICATION NUMBER: US/10/277,161
; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 60/192,586
; PRIOR FILING DATE: 2000-03-28

; PRIOR APPLICATION NUMBER: 60/203,343
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 60/263,226
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/271,426
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/818,991
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 73
; LENGTH: 5887
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-277-161-73

Query Match 13.0%; Score 122.4; DB 15; Length 5887;
Best Local Similarity 79.7%; Pred. No. 5.1e-26;
Matches 169; Conservative 0; Mismatches 41; Indels 2; Gaps 2;

QY 445 GGGATTGGCAGGATGGCTTCAGAT-GGGCTGAAACCCCTGCCGCTATTATTTAAACTG 503
Db 3830 GAGATTGGCAGGATGGCTTCAGATGGGCTGAAACGCTGCCGCTATTATTTAAACTG 3889
QY 504 GTTCTCTGTGAGAGCTGTGAATCGGCTCTGTATGCGCTTGAGAAAAGCCCATTCATG 563
Db 3890 GTTCTCTGAGAGACCTGTGAATCGGCTCTGTGCGCTCGAGAAAAGCCCATTCATG 3949
QY 564 AGAGGCAAGCCAGTGGG-TCCCCAACTCCCGACCCCGCTCTCCCAATGACAGC 622
Db 3950 AGAGGAGGTCCAGTGGGTCTCTCGTACTTCCAGACCCCGCTCTCCCAATGCCCCC 4009
QY 623 CTCGCCGCTCATCCCCCCCCCCCCCCCCCG 654
Db 4010 TGTGCCGCGCGCGCCACCTCTCGGCTCCAG 4041

RESULT 6

US-09-847-101B-28
; Sequence 28, Application US/09847101B
; Publication No. US2002019327A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: FRIEDLANDER, MARTIN
; TITLE OF INVENTION: VECTORS FOR OCULAR TRANSDUCTION AND USE THEREFOR FOR GENETIC THER
; FILE REFERENCE: 22908-1226B
; CURRENT APPLICATION NUMBER: US/09/847,101B
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/562,934
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 1240
; TYPE: DNA
; ORGANISM: adenovirus
US-09-847-101B-28

Query Match 11.1%; Score 104.4; DB 9; Length 1240;
Best Local Similarity 99.1%; Pred. No. 8.3e-21;
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 757 TGTAGGGCGCAGTAGTCCAGGTTTCTTGATCATGTCATCTATCTGTCCTCTTTT 816
Db 1001 TTAGGGCCAGTAGTCCAGGTTTCTTGATCATGTCATCTATCTGTCCTCTTTT 1060
QY 817 TTCCACAGCTCGCGTTGAGGCAAACTCTTCGCGTCTTTCCAGT 862
Db 1061 TTCCACAGCTCGCGTTGAGGCAAACTCTTCGCGTCTTTCCAGT 1106

RESULT 7

```
US-09-482-682-32
; Sequence 32, Application US/09482682
; Publication No. US20030157688A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: HALLENBECK, PAUL
; APPLICANT: STEVENSON, SUSAN
; APPLICANT: SKRIPCHENKO, YELENA
; TITLE OF INVENTION: ADENOVIRUS VECTORS, PACKAGING CELL LINES, COMPOSITIONS,
; TITLE OF INVENTION: AND METHODS FOR PREPARATION AND USE
; FILE REFERENCE: 1294.0010001
; CURRENT APPLICATION NUMBER: US/09/482,682
; CURRENT FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 1240
; TYPE: DNA
; ORGANISM: adenovirus
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-482-682-32

Query Match 11.1%; Score 104.4; DB 10; Length 1240;
Best Local Similarity 99.1%; Pred. No. 8.3e-21; Indels 0; Gaps 0;
Matches 105; Conservative 0; Mismatches 1;

QY 757 TGTAGGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATATCTATCTGTCCTCTTTT 816
Db 1001 TCTAGGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATATCTATCTGTCCTCTTTT 1060

QY 817 TTCCACAGCTCGCGTTGAGGACAACTCTTCGCGGTCTTTCCAGT 862
Db 1061 TTCCACAGCTCGCGTTGAGGACAACTCTTCGCGGTCTTTCCAGT 1106

RESULT 8
US-09-847-101B-42
; Sequence 42, Application US/09847101B
; Publication No. US20020193327A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: FRIEDLANDER, MARTIN
; TITLE OF INVENTION: VECTORS FOR OCULAR TRANSDUCTION AND USE THEREFOR FOR GENETIC THER
; FILE REFERENCE: 22908-1226B
; CURRENT APPLICATION NUMBER: US/09/847,101B
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/562,934
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 7231
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid pdV80
US-09-847-101B-42

Query Match 11.1%; Score 104.4; DB 9; Length 7231;
Best Local Similarity 99.1%; Pred. No. 1.3e-20; Indels 0; Gaps 0;
Matches 105; Conservative 0; Mismatches 1;

QY 757 TGTAGGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATATCTGTCCTCTTTT 816
Db 1849 TCTAGGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATATCTGTCCTCTTTT 1908

QY 817 TTCCACAGCTCGCGTTGAGGACAACTCTTCGCGGTCTTTCCAGT 862
Db 1909 TTCCACAGCTCGCGTTGAGGACAACTCTTCGCGGTCTTTCCAGT 1954

RESULT 9
US-09-847-101B-42
; Sequence 42, Application US/09847101B
; Publication No. US20020193327A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: FRIEDLANDER, MARTIN
; TITLE OF INVENTION: VECTORS FOR OCULAR TRANSDUCTION AND USE THEREFOR FOR GENETIC THER
; FILE REFERENCE: 22908-1226B
; CURRENT APPLICATION NUMBER: US/09/847,101B
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/562,934
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 7231
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid pdV80
US-09-847-101B-42

Query Match 11.1%; Score 104.4; DB 9; Length 7231;
Best Local Similarity 99.1%; Pred. No. 1.3e-20; Indels 0; Gaps 0;
Matches 105; Conservative 0; Mismatches 1;

QY 757 TGTAGGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATATCTGTCCTCTTTT 816
Db 1849 TCTAGGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATATCTGTCCTCTTTT 1908

QY 817 TTCCACAGCTCGCGTTGAGGACAACTCTTCGCGGTCTTTCCAGT 862
Db 1909 TTCCACAGCTCGCGTTGAGGACAACTCTTCGCGGTCTTTCCAGT 1954

US-09-482-682-64
; Sequence 64, Application US/09482682
; Publication No. US20030157688A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: HALLENBECK, PAUL
; APPLICANT: STEVENSON, SUSAN
; APPLICANT: SKRIPCHENKO, YELENA
; TITLE OF INVENTION: ADENOVIRUS VECTORS, PACKAGING CELL LINES, COMPOSITIONS,
; TITLE OF INVENTION: AND METHODS FOR PREPARATION AND USE
; FILE REFERENCE: 1294.0010001
; CURRENT APPLICATION NUMBER: US/09/482,682
; CURRENT FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 7231
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-482-682-64

Query Match 11.1%; Score 104.4; DB 10; Length 7231;
Best Local Similarity 99.1%; Pred. No. 1.3e-20; Indels 0; Gaps 0;
Matches 105; Conservative 0; Mismatches 1;

QY 757 TGTAGGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATATCTGTCCTCTTTT 816
Db 1849 TCTAGGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATATCTGTCCTCTTTT 1908

QY 817 TTCCACAGCTCGCGTTGAGGACAACTCTTCGCGGTCTTTCCAGT 862
Db 1909 TTCCACAGCTCGCGTTGAGGACAACTCTTCGCGGTCTTTCCAGT 1954

RESULT 10
US-09-847-101B-30
; Sequence 30, Application US/09847101B
; Publication No. US20020193327A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: FRIEDLANDER, MARTIN
; TITLE OF INVENTION: VECTORS FOR OCULAR TRANSDUCTION AND USE THEREFOR FOR GENETIC THER
; FILE REFERENCE: 22908-1226B
; CURRENT APPLICATION NUMBER: US/09/847,101B
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/562,934
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 7960
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid pdV67
US-09-847-101B-30

Query Match 11.1%; Score 104.4; DB 9; Length 7960;
Best Local Similarity 99.1%; Pred. No. 1.3e-20; Indels 0; Gaps 0;
Matches 105; Conservative 0; Mismatches 1;

QY 757 TGTAGGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATATCTGTCCTCTTTT 816
Db 1929 TCTAGGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATATCTGTCCTCTTTT 1988

QY 817 TTCCACAGCTCGCGTTGAGGACAACTCTTCGCGGTCTTTCCAGT 862
Db 1989 TTCCACAGCTCGCGTTGAGGACAACTCTTCGCGGTCTTTCCAGT 2034
```

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RESULT 11
US-09-482-682-44
; Sequence 44, Application US/09482682
; Publication No. US20030157688A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: HALLENBECK, PAUL
; APPLICANT: STEVENSON, SUSAN
; APPLICANT: SKRIPCHENKO, YELENA
; TITLE OF INVENTION: ADENOVIRUS VECTORS, PACKAGING CELL LINES, COMPOSITIONS,
; TITLE OF INVENTION: AND METHODS FOR PREPARATION AND USE
; FILE REFERENCE: 1294.0010001
; CURRENT APPLICATION NUMBER: US/09/482,682
; CURRENT FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 44
; LENGTH: 7960
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-482-682-44

Query Match          11.1%; Score 104.4; DB 10; Length 7960;
Best Local Similarity 99.1%; Pred. No. 1.3e-20;
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      757 TGTAGGCGCAGTAGTCACGGGTTTCCTTGATGATGTCATACCTATCTGTCCTCTTTT 816
Db      1929 TCTAGGCGCAGTAGTCACGGGTTTCCTTGATGATGTCATACCTATCTGTCCTCTTTT 1988

QY      817 TTCCACAGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTCCAGT 862
Db      1989 TTCCACAGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTCCAGT 2034

RESULT 12
US-09-847-101B-33
; Sequence 33, Application US/09847101B
; Publication No. US20020193327A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: FRIEDLANDER, MARTIN
; TITLE OF INVENTION: VECTORS FOR OCULAR TRANSDUCTION AND USE THEREFOR FOR GENETIC THER
; FILE REFERENCE: 22908-1226B
; CURRENT APPLICATION NUMBER: US/09/847,101B
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/562,934
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 7989
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 4242
; OTHER INFORMATION: N is any
; NAME/KEY: misc_feature
; LOCATION: 4245
; OTHER INFORMATION: N is any
; OTHER INFORMATION: Description of Artificial Sequence: plasmid pDV69
US-09-847-101B-33

Query Match          11.1%; Score 104.4; DB 9; Length 7989;
Best Local Similarity 99.1%; Pred. No. 1.3e-20;
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      757 TGTAGGCGCAGTAGTCACGGGTTTCCTTGATGATGTCATACCTATCTGTCCTCTTTT 816
Db      1929 TCTAGGCGCAGTAGTCACGGGTTTCCTTGATGATGTCATACCTATCTGTCCTCTTTT 1988

QY      817 TTCCACAGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTCCAGT 862
Db      1989 TTCCACAGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTCCAGT 2034

RESULT 13
US-09-482-682-47
; Sequence 47, Application US/09482682
; Publication No. US20030157688A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: HALLENBECK, PAUL
; APPLICANT: STEVENSON, SUSAN
; APPLICANT: SKRIPCHENKO, YELENA
; TITLE OF INVENTION: ADENOVIRUS VECTORS, PACKAGING CELL LINES, COMPOSITIONS,
; TITLE OF INVENTION: AND METHODS FOR PREPARATION AND USE
; FILE REFERENCE: 1294.0010001
; CURRENT APPLICATION NUMBER: US/09/482,682
; CURRENT FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 7989
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-482-682-47

Query Match          11.1%; Score 104.4; DB 10; Length 7989;
Best Local Similarity 99.1%; Pred. No. 1.3e-20;
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      757 TGTAGGCGCAGTAGTCACGGGTTTCCTTGATGATGTCATACCTATCTGTCCTCTTTT 816
Db      1929 TCTAGGCGCAGTAGTCACGGGTTTCCTTGATGATGTCATACCTATCTGTCCTCTTTT 1988

QY      817 TTCCACAGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTCCAGT 862
Db      1989 TTCCACAGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTCCAGT 2034

RESULT 14
US-09-847-101B-29
; Sequence 29, Application US/09847101B
; Publication No. US20020193327A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: FRIEDLANDER, MARTIN
; TITLE OF INVENTION: VECTORS FOR OCULAR TRANSDUCTION AND USE THEREFOR FOR GENETIC THER
; FILE REFERENCE: 22908-1226B
; CURRENT APPLICATION NUMBER: US/09/847,101B
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/562,934
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 8383
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid pDV60
US-09-847-101B-29

Query Match          11.1%; Score 104.4; DB 9; Length 8383;
Best Local Similarity 99.1%; Pred. No. 1.4e-20;
```

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QY      757 TGTAGGCGCAGTAGTCACGGGTTTCCTTGATGATGTCATACCTATCTGTCCTCTTTT 816
Db      1929 TCTAGGCGCAGTAGTCACGGGTTTCCTTGATGATGTCATACCTATCTGTCCTCTTTT 1988

QY      817 TTCCACAGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTCCAGT 862
Db      1989 TTCCACAGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTCCAGT 2034

RESULT 13
US-09-482-682-47
; Sequence 47, Application US/09482682
; Publication No. US20030157688A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: HALLENBECK, PAUL
; APPLICANT: STEVENSON, SUSAN
; APPLICANT: SKRIPCHENKO, YELENA
; TITLE OF INVENTION: ADENOVIRUS VECTORS, PACKAGING CELL LINES, COMPOSITIONS,
; TITLE OF INVENTION: AND METHODS FOR PREPARATION AND USE
; FILE REFERENCE: 1294.0010001
; CURRENT APPLICATION NUMBER: US/09/482,682
; CURRENT FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 7989
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-482-682-47

Query Match          11.1%; Score 104.4; DB 10; Length 7989;
Best Local Similarity 99.1%; Pred. No. 1.3e-20;
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      757 TGTAGGCGCAGTAGTCACGGGTTTCCTTGATGATGTCATACCTATCTGTCCTCTTTT 816
Db      1929 TCTAGGCGCAGTAGTCACGGGTTTCCTTGATGATGTCATACCTATCTGTCCTCTTTT 1988

QY      817 TTCCACAGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTCCAGT 862
Db      1989 TTCCACAGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTCCAGT 2034

RESULT 14
US-09-847-101B-29
; Sequence 29, Application US/09847101B
; Publication No. US20020193327A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: FRIEDLANDER, MARTIN
; TITLE OF INVENTION: VECTORS FOR OCULAR TRANSDUCTION AND USE THEREFOR FOR GENETIC THER
; FILE REFERENCE: 22908-1226B
; CURRENT APPLICATION NUMBER: US/09/847,101B
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/562,934
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 8383
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid pDV60
US-09-847-101B-29

Query Match          11.1%; Score 104.4; DB 9; Length 8383;
Best Local Similarity 99.1%; Pred. No. 1.4e-20;
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Mon Sep 13 07:48:12 2004

	Matches	105;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	757	TGTAGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATACCTATCTGTCCTCTTTT	816							
Db	1907	TCTAGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATACCTATCTGTCCTCTTTT	1966							
QY	817	TTCCACAGCTCGCGGTTGAGGACAACTCTTCGCGGTCTTTCCAGT	862							
Db	1967	TTCCACAGCTCGCGGTTGAGGACAACTCTTCGCGGTCTTTCCAGT	2012							

RESULT 15
 US-09-482-682-43
 ; Sequence 43, Application US/09482682
 ; Publication No. US20030157688A1
 ; GENERAL INFORMATION:
 ; APPLICANT: VON SEGHERN, DANIEL
 ; APPLICANT: NEMEROW, GLEN R.
 ; APPLICANT: HALLENBECK, PAUL
 ; APPLICANT: STEVENSON, SUSAN
 ; APPLICANT: SKRIPCHENKO, YELENA
 ; TITLE OF INVENTION: ADENOVIRUS VECTORS, PACKAGING CELL LINES, COMPOSITIONS,
 ; TITLE OF INVENTION: AND METHODS FOR PREPARATION AND USE
 ; FILE REFERENCE: 1294.0010001
 ; CURRENT APPLICATION NUMBER: US/09/482,682
 ; CURRENT FILING DATE: 2000-01-14
 ; NUMBER OF SEQ ID NOS: 76
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 43
 ; LENGTH: 8383
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: plasmid
 US-09-482-682-43

Query Match	11.1%	Score	104.4;	DB	10;	Length	8383;
Best Local Similarity	99.1%	Pred. No.	1.4e-20;				
Matches	105;	Conservative	0;	Mismatches	1;	Indels	0;
Gaps	0;						
QY	757	TGTAGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATACCTATCTGTCCTCTTTT	816				
Db	1907	TCTAGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATACCTATCTGTCCTCTTTT	1966				
QY	817	TTCCACAGCTCGCGGTTGAGGACAACTCTTCGCGGTCTTTCCAGT	862				
Db	1967	TTCCACAGCTCGCGGTTGAGGACAACTCTTCGCGGTCTTTCCAGT	2012				

Search completed: September 11, 2004, 14:11:20
 Job time : 917.647 secs

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OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 09:20:47 ; Search time 322.028 Seconds
(without alignments)
5187.326 Million cell updates/sec

Title: US-09-808-388-6

Perfect score: 332

Sequence: 1 gtaccaattgcacaaacta.....caactctggagctctctgag 332

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 6608766

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
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6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
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8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10C_NEW_PUB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10C_NEW_PUB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US10C_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	332	100.0	332	9	US-09-808-388-6
2	271	81.6	271	9	US-09-808-388-5
3	213	64.2	1080	10	US-09-865-866-17
4	165	49.7	6083	13	US-10-221-714A-440
5	150.2	45.2	6083	13	US-10-221-714A-439
6	118.8	35.8	967	15	US-10-210-120-75
7	84.4	25.4	3330	9	US-09-917-800A-1495
8	84.4	25.4	3330	12	US-10-152-319A-2157
9	84.4	25.4	3330	16	US-10-191-803-398
10	80.8	24.3	1076	9	US-09-925-300-70
11	50	15.1	735	9	US-09-981-353-17
12	49.6	14.9	4990	10	US-09-865-866-97
13	41	12.3	41	9	US-09-808-388-3
14	34.2	10.3	371	15	US-10-387-495-8
15					Sequence 6, Appli
					Sequence 5, Appli
					Sequence 17, Appl
					Sequence 440, App
					Sequence 439, App
					Sequence 75, Appl
					Sequence 1495, Ap
					Sequence 2157, Ap
					Sequence 398, App
					Sequence 70, Appl
					Sequence 17, Appl
					Sequence 97, Appl
					Sequence 3, Appli
					Sequence 8, Appli

c	15	34.2	10.3	742	13	US-10-027-632-151276	Sequence 151276,
c	16	34.2	10.3	742	16	US-10-027-632-151276	Sequence 151276,
	17	33.8	10.2	420	15	US-10-422-264-17	Sequence 17, Appl
	18	33.8	10.2	1441	15	US-10-422-264-13	Sequence 13, Appl
	19	33.8	10.2	2136	9	US-09-862-658-3	Sequence 3, Appli
	20	33.8	10.2	2136	15	US-10-175-696-24	Sequence 24, Appl
	21	33.8	10.2	2136	17	US-10-776-871-24	Sequence 24, Appl
	22	33.8	10.2	2236	15	US-10-422-264-5	Sequence 5, Appli
	23	33.8	10.2	2307	13	US-10-302-172-803	Sequence 803, App
	24	33.8	10.2	2604	15	US-10-422-264-23	Sequence 23, Appli
	25	33.8	10.2	2701	15	US-10-422-264-1	Sequence 1, Appli
	26	33.8	10.2	3320	9	US-09-862-658-1	Sequence 1, Appli
	27	33.8	10.2	3320	15	US-10-175-696-22	Sequence 22, Appl
	28	33.8	10.2	3320	17	US-10-776-871-22	Sequence 22, Appl
	29	33.8	10.2	3384	15	US-10-422-264-29	Sequence 29, Appl
	30	33.2	10.0	2835	16	US-10-104-047-1501	Sequence 1501, Ap
c	31	33	9.9	343	17	US-10-767-701-23550	Sequence 23550, A
	32	32.6	9.8	54552	13	US-10-087-192-1303	Sequence 1303, Ap
	33	32.4	9.8	819	13	US-10-027-632-130312	Sequence 130312,
c	34	32.4	9.8	819	16	US-10-027-632-130312	Sequence 130312,
	35	32.4	9.8	94529	16	US-10-034-650-52	Sequence 52, Appl
	36	32.2	9.7	573	13	US-10-027-632-50048	Sequence 50048, A
	37	32.2	9.7	573	13	US-10-027-632-50049	Sequence 50049, A
	38	32.2	9.7	573	13	US-10-027-632-69880	Sequence 69880, A
	39	32.2	9.7	573	13	US-10-027-632-69881	Sequence 69881, A
	40	32.2	9.7	573	13	US-10-027-632-70565	Sequence 70565, A
	41	32.2	9.7	573	13	US-10-027-632-70566	Sequence 70566, A
	42	32.2	9.7	573	16	US-10-027-632-50048	Sequence 50048, A
	43	32.2	9.7	573	16	US-10-027-632-50049	Sequence 50049, A
	44	32.2	9.7	573	16	US-10-027-632-69880	Sequence 69880, A
	45	32.2	9.7	573	16	US-10-027-632-69881	Sequence 69881, A

ALIGNMENTS

RESULT 1

US-09-808-388-6

; Sequence 6, Application US/09808388

; Patent No. US20020081719A1

; GENERAL INFORMATION:

; APPLICANT: Massaad, Charbel

; APPLICANT: Berenbaum, Francis

; APPLICANT: Olivier, Jean-Luc

; APPLICANT: Salvat, Colette

; APPLICANT: Bereziat, Gilbert

; TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising them

; TITLE OF INVENTION: their uses

; FILE REFERENCE: ST00010

; CURRENT APPLICATION NUMBER: US/09/808,388

; CURRENT FILING DATE: 2001-09-20

; PRIOR APPLICATION NUMBER: FR/00/03262

; PRIOR FILING DATE: 2000-03-14

; PRIOR APPLICATION NUMBER: US 60/196,959

; PRIOR FILING DATE: 2000-04-13

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 6

; LENGTH: 332

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: PPPE/PLA2s hybrid promoter

US-09-808-388-6

Query Match 100.0%; Score 332; DB 9; Length 332;

Best Local Similarity 100.0%; Pred. No. 1.8e-106;

Matches 332; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTACCAATTCGACAAACTAGTCAAGGTCAATCAAACTAGTCAAGGTCAAGTCAAAATCGA 60

Db 1 GTACCAATTCGACAAACTAGTCAAGGTCAATCAAACTAGTCAAGGTCAAAATCGA 60

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QY 61 ACGCGCAAACTGCCTGAAATGTGTTTGGCATCAGTACTGACAGTAAGGTTTCCCA 120
Db 61 ACGCGCAAACTGCCTGAAATGTGTTTGGCATCAGTACTGACAGTAAGGTTTCCCA 120
QY 121 ATCTCAACTCTGTCCTGCAGCTGATGAGGGGAGGAAAGGATTACCTAGGGGTATGG 180
Db 121 ATCTCAACTCTGTCCTGCCAGCTGATGAGGGGAGGAAAGGATTACCTAGGGGTATGG 180
QY 181 GCGACCAATCTGAGTCCACCACTGACAGCGCCCATCCCCAGCCTTGTGCTCACCTAC 240
Db 181 GCGACCAATCTGAGTCCACCACTGACAGCGCCCATCCCCAGCCTTGTGCTCACCTAC 240
QY 241 CCCCAACTCTCCAGAGGAGCAGCTATTATTAGGGGAGCAGGAGTGCAGAACAAACAGAC 300
Db 241 CCCCAACTCTCCAGAGGAGCAGCTATTATTAGGGGAGCAGGAGTGCAGAACAAACAGAC 300
QY 301 GGCCTGGGGATACAACTCTGAGTCCTCTGAG 332
Db 301 GGCCTGGGGATACAACTCTGAGTCCTCTGAG 332

RESULT 2
US-09-808-388-5
; Sequence 5, Application US/09808388
; Patent No. US20020081719A1
; GENERAL INFORMATION:
; APPLICANT: Massaad, Charbel
; APPLICANT: Berenbaum, Francis
; APPLICANT: Olivier, Jean-Luc
; APPLICANT: Salvat, Colette
; APPLICANT: Berezat, Gilbert
; TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising them
; TITLE OF INVENTION: their uses
; FILE REFERENCE: ST00010
; CURRENT APPLICATION NUMBER: US/09/808,388
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: FR/00/03262
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/196,959
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 5
; LENGTH: 271
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fragment of the PLA2s promoter
US-09-808-388-5
Query Match 81.6%; Score 271; DB 9; Length 271;
Best Local Similarity 100.0%; Pred. No. 5.6e-85;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 62 CGCGGCAAACTGCCTGAAATGTGTTTGGCATCAGTACTGACAGTAAGGTTTCCCA 121
Db 1 CGCGGCAAACTGCCTGAAATGTGTTTGGCATCAGTACTGACAGTAAGGTTTCCCA 60
QY 122 TCCTCAACTCTGTCCTGCAGCTGATGAGGGGAGGAAAGGATTACCTAGGGGTATGG 181
Db 61 TCCTCAACTCTGTCCTGCCAGCTGATGAGGGGAGGAAAGGATTACCTAGGGGTATGG 120
QY 182 CGACCAATCTGAGTCCACCACTGACAGCGCCCATCCCCAGCCTTGTGCTCACCTACC 241
Db 121 CGACCAATCTGAGTCCACCACTGACAGCGCCCATCCCCAGCCTTGTGCTCACCTACC 180
QY 242 CCCCAACTCTCCAGAGGAGCAGCTATTATTAGGGGAGCAGGAGTGCAGAACAAACAGAC 301
Db 181 CCCCAACTCTCCAGAGGAGCAGCTATTATTAGGGGAGCAGGAGTGCAGAACAAACAGAC 240
QY 302 GGCCTGGGGATACAACTCTGAGTCCTCTGAG 332
Db 241 GGCCTGGGGATACAACTCTGAGTCCTCTGAG 271
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RESULT 3
US-09-865-866-17
; Sequence 17, Application US/09865866
; Publication No. US20030045487A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EXH
; FILE REFERENCE: RTS-0221
; CURRENT APPLICATION NUMBER: US/09/865,866
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 17
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-865-866-17
Query Match 64.2%; Score 213; DB 10; Length 1080;
Best Local Similarity 93.1%; Pred. No. 3e-64;
Matches 256; Conservative 0; Mismatches 15; Indels 4; Gaps 3;
QY 61 ACGCGCAAACTGCCTGAAATGTGTTTGGCATCAGTACTGACAGTAAGG-TTTCCC 119
Db 762 ACTCGGCAAACTGCCTGAATGTGTTTGGCATCAGGCTACTGACACGTAAGGGTTTCCC 821
QY 120 AATCCTCAACTCTGTCTGTG--CCAGCTGATGAGGGGAGGAAAGGATTACCTAGGGTA 177
Db 822 AATCCTCAACTCTGTCTGTGGCAGGCTGATGAGGGGAGGAAAGGATTACCTAGGGTA 881
QY 178 TGGGGGACCAATCCTGAGTCCACCACTGACACGCCCATCCCCAGCCTTGTGCTCAC 237
Db 882 TGGGGGACCAATCCTGAGTCCACCACTGACACGCCCATCCCCAGCCTTGTGCTCAC 941
QY 238 TACCCCCAACCTCCAGAGGAGCAGCTATTATTAGGGGAGCAGGAGTGCAGAACAA 297
Db 942 TACCCCCAACCT-CCAGAGGAGCAGCTATTATTAGGGGAGCAGGAGTGCAGAACAA 1000
QY 298 GACGGCCTGGGGATACAACTCTGGAGTCCTCTGAG 332
Db 1001 GACGGCCTGGGGATACAACTCTGGAGTCCTCTGAG 1035

RESULT 4
US-10-221-714A-440/c
; Sequence 440, Application US/10221714A
; Publication No. US20040048254A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; TITLE OF INVENTION: tumor suppressor genes and oncogenes
; FILE REFERENCE: 5013,1005
; CURRENT APPLICATION NUMBER: US/10/221,714A
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: PCT/EP01/02955
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: DE 10013847.0
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 540
; SEQ ID NO 440
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; LENGTH: 6083
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-221-714A-440

Query Match          49.7%; Score 165; DB 13; Length 6083;
Best Local Similarity 74.7%; Pred. No. 5.7e-47;
Matches 207; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 55 ATTGGAAGCGGCAAACTGCTGAAATGTGTTTGGCATCAGCTACTGACACGTAAGGT 114
D 1336 ATAAAAAACTACAAAACCTACTTAAATATATTTTAACTCACTACTTAAACGCTAAAT 1277
QY 115 TTCCCAATCCTCAACTCTGCTGCGCAGCTGATGAGGGAAGGAGGATTACCTAGG 174
D 1276 TTCCCAATCCTCAACTCTGCTGCGCAGCTGATGAGGGAAGGAGGATTACCTAGG 174
QY 175 GTATGGGCGACCAATCCTGAGTCCACCACTGACACGCCCATCCCGAGCCTTGTGCTC 234
D 1216 ATATAAGGACCAATCTTAATTCACCACTAACCCGCCCATCCCGAGCCTTGTGCTC 1157
QY 235 ACCTACCCCACTCCAGAGGAGGAGCTATTTAAGGGGAGGAGGAGTGCAGAACAA 294
D 1156 ACCTACCCCACTCCAGAGGAGGAGCTATTTAAGGGGAGGAGGAGTGCAGAACAA 1097
QY 295 CAAGACGGCTGGGATACAACTCTGGAGTCTCTGA 331
D 1096 CAAGACGGCTGGGATACAACTCTGGAGTCTCTGA 1060

RESULT 5
US-10-221-714A-439
; Sequence 439, Application US/10221714A
; Publication No. US20040048254A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; FILE REFERENCE: 5013.1005
; CURRENT APPLICATION NUMBER: US/10/221,714A
; CURRENT FILING DATE: 2003-01-21
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: DE 10013847.0
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 540
; SEQ ID NO 439
; LENGTH: 6083
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-221-714A-439

Query Match          45.2%; Score 150.2; DB 13; Length 6083;
Best Local Similarity 72.7%; Pred. No. 9.5e-42;
Matches 194; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 66 GCNAACCTGCTGAATGTGTTTGGCATCAGCTACTGACACGTAAGGTTTCCCAATCCT 125
D 4759 GTAAAAATGTTGAAATGTGTTTGGTATTAGTTATTGATACGTAAGGTTTATTATTT 4818
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QY 126 CAATCTCTCTCGCAGCTGATGAGGGAAGAAAGGATTAACCTAGGCTTATGGCGAC 185
D 4819 TAAATTTGTTTGTAGTTGATGAGGGGAAGAAAGGATTAATTTAGGGGTATGGCGAT 4878
QY 186 CAATCTCTGAGTCCCACTGACACGCCCATCCCGAGCCTTGTGCTCACCCTACCCCA 245
D 4879 TAAATTTGAGTTTAAATGATTACGTTTATTTTAGTTTGTGTTTATTTATTTT 4938
QY 246 ACCTCCCAAGAGGAGCAGCTATTTAAGGGGAGGAGTGCAGACAAACAGACGGCT 305
D 4939 ATTTTATAGGGAGTAGTTATTTAAGGGGAGTAGGAGTAGAATAAATAAGACGGTT 4998
QY 306 GGGATACAACTCTGGAGTCTCTGAG 332
D 4999 GGGATATAATTTGGAGTTTTTTGAG 5025

RESULT 6
US-10-210-120-75
; Sequence 75, Application US/10210120
; Publication No. US20030175736A1
; GENERAL INFORMATION:
; APPLICANT: Chinnaiyan, Arul M.
; APPLICANT: Rubin, Mark A.
; APPLICANT: Sreekumar, Arun
; TITLE OF INVENTION: Expression Profile of Prostate Cancer
; FILE REFERENCE: UM-07221
; CURRENT APPLICATION NUMBER: US/10/210,120
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 60/309,581
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/334,468
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 75
; LENGTH: 967
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-210-120-75

Query Match          35.8%; Score 118.8; DB 15; Length 967;
Best Local Similarity 83.3%; Pred. No. 5.1e-31;
Matches 135; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 171 AGGGGTATGGCGACCAATCCTGAGTCCCACTGACACGCCCATCCCGAGCCTTGTG 230
D 3 AGGAAAAGAGCAACAGATCCAGGAGCATTCACCTGCTCTCCAAACAGCCTTGTG 62
QY 231 CTTCACTACCTACCCCAACCTCCAGAGGAGCAGCTATTTAAGGGGAGCAGGAGTGAGAA 290
D 63 CTTCACTACCTACCCCAACCTCCAGAGGAGCAGCTATTTAAGGGGAGCAGGAGTGAGAA 122
QY 291 CAACAGAGCGCTGGGATACAACTCTGGAGTCTCTGAG 332
D 123 CAACAGAGCGCTGGGATACAACTCTGGAGTCTCTGAG 164

RESULT 7
US-09-917-800A-1495
; Sequence 1495, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Blashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
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CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,980
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1495
LENGTH: 3330
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020119462A1 X51529
US-09-917-800A-1495

Query Match 25.4%; Score 84.4; DB 9; Length 3330;
Best Local Similarity 64.9%; Pred. No. 1.2e-18;
Matches 157; Conservative 0; Mismatches 81; Indels 4; Gaps 2;

QY 67 CAAACTGCGCTGAATGTGTTTGGCATCAGCTACTGCACAGTAAGGTTTCCTCAATCCCTC 126
Db 260 CGAAATCAGCTAAAGTTTATGATGCCCACAAACCATTGTTAGAGGGCTTTTTCCGGCCCTC 319

QY 127 AACTCTGTCTCCAGCTGATGAGGGGAAGAAGGATTAACCTAGGGGTATGG--CGA 184
Db 320 AAGGCTGTCTCGCAGCTGTGTTGGGGGAAAAGGGGAAATTAACCGAGGCGTTGGGTATGC 379

QY 185 CCAATCTGAGTCCACAACCTGACACAGCCCCA--TCGCCGCTTGTCCTCACTACCC 242
Db 380 CCGTCTGTGAATCCATTATTTGGCCACACCCCACCTCCCCTGCTCTCGATCC 439

QY 243 CCACCTCCCGAGGAGCAGCTATTTAAGGGAGCAGAGTGCAGACAACAACAGCGG 302
Db 440 CCAGCCCTCGCAGAGGAAGAGCTATTTAAGAGCATTTGGGAGTACAGGHAACAAGGCAG 499

QY 303 CC 304
|
Db 500 GC 501

RESULT 8
US-10-152-319A-2157
Sequence 2157, Application US/10152319A
Publication No. US20040072160A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Higgs, Brandon
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
TITLE OF INVENTION: Molecular
FILE REFERENCE: 44921-5089-US
CURRENT APPLICATION NUMBER: US/10152,319A
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: US 60/292,335
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/297,523
PRIOR FILING DATE: 2001-06-13
Toxicology Modeling


```
; PRIOR APPLICATION NUMBER: US 60/377,611
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 1140
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 398
; LENGTH: 3330
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20040014040A1 X51529
US-10-191-803-398

Query Match      25.4%; Score 84.4; DB 16; Length 3330;
Best Local Similarity 64.9%; Pred. No. 1.2e-18;
Matches 157; Conservative 0; Mismatches 81; Indels 4; Gaps 2;

QY 67 CAAACTGCTGAAATGTTTGGCATCAGCTACTGACACCGTAAGGTTTCCCAATCCTC 126
Db |||||
260 CGAATCAGCTAAAGTTATGATGCGCACCAACCCATGGTATGAGGCTTTCCGGCCCTC 319
QY 127 AACTCTGCTCCAGCTGATGAGGGGAAGAAAGGATTACTAGGGGTATGG--CGA 184
Db |||||
320 AAGGCTGTCTCCAGCTGTTGGGGGAAAGGGGAAATTACCCAGGGGTTGGGTATGC 379
QY 185 CCAATCTTGAGTCCCACTCAACCAAGCCCA--TCCCCAGCTTGTGCTCACCTACCC 242
Db |||||
380 CGTCTGTAATCCATTATTGGCCACACCCACCTCCCTGCTGCTCTCCGATCC 439
QY 243 CCAACTCTCCAGGAGGAGCAGCTATTTTAAGGGGAGCAGGTGCAGAACAAACAAGCGG 302
Db |||||
440 CCAGCCCTGCAGAGGGAAGAGCTATTTAAGAGCATTTGGGAGTACAGGAAACAAAGCGAC 499
QY 303 CC 304
Db |
500 GC 501

RESULT 10
US-09-925-300-70
; Sequence 70, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 70
; LENGTH: 1076
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (911)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-70

Query Match      24.3%; Score 80.8; DB 9; Length 1076;
Best Local Similarity 95.3%; Pred. No. 1.4e-17;
Matches 82; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 247 CTCCAGAGGAGCAGCTATTTAAGGGAGCAGGAGTGCGAGAACAAACAAGCGGCTG 306
Db |||||
2 CCAACAGAGGAGCAGCTATTTAAGGGAGCAGGAGTGCGAGAACAAACRAGACGCGCTG 61
QY 307 GGGATACAACTCTGGAGTCTCTGAG 332
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Db 62 GGGATACAACTCTGGAGTCTCTGAG 87

RESULT 11
US-09-981-353-17
; Sequence 17, Application US/09981353
; Patent No. US20020160382A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; APPLICANT: Jones, David A.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0039 US
; CURRENT APPLICATION NUMBER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 17
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 474322.36
; NAME/KEY: unsure
; LOCATION: 388
; OTHER INFORMATION: a, t, c, g, or other
US-09-981-353-17

Query Match      15.1%; Score 50; DB 9; Length 735;
Best Local Similarity 100.0%; Pred. No. 8.7e-07;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 283 GTGCAGAACAAACAAGACGGCTGGGGATACAACTCTCGAGTCTCTGAG 332
Db |||||
1 GTGCAGAACAAACAAGACGGCTGGGGATACAACTCTCGAGTCTCTGAG 50

RESULT 12
US-09-865-866-97
; Sequence 97, Application US/09865866
; Publication No. US20030045487A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
; FILE REFERENCE: RTS-0221
; CURRENT APPLICATION NUMBER: US/09/865,866
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 97
; LENGTH: 4990
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2026)...(2068)
; NAME/KEY: CDS
; LOCATION: (2245)...(2389)
; NAME/KEY: CDS
; LOCATION: (2622)...(2731)
; NAME/KEY: CDS
; LOCATION: (4098)...(4240)
US-09-865-866-97

Query Match      14.9%; Score 49.6; DB 10; Length 4990;
Best Local Similarity 59.4%; Pred. No. 2.8e-06;
Matches 139; Conservative 0; Mismatches 64; Indels 31; Gaps 2;

QY 67 CAAAACTCCCTGAATGTGTTTGGCATCAGCTACTGACAGTAAAGTTTCCCAATCCTC 126
Db |||||
1016 CAAATACAGCTGAATTTATGATGCGGCACCCCTTGTGATGAGGCTTTTCCAGCCCTC 1075
```

```
QY 127 AACTCTGTCTCCAGCTGATGAGGGGAAGGATTAACCTAGGGGTATGGCGACC 186
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1076 AGGGCTGCCCTGCCAGCTGTGTGGGAACAAAGGAGCATTTGGGTATGC-----CC 1125
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 187 AATCCTGAGTCCACCAACTGACACAGCCCATCCCGAGCCTTGTGCCTCACTACCCCAA 246
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1126 ATCCGTGATCCACTATTGACACACACCCACCT-----CCCCAT 1164
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 247 CTTCCAGAGGGAGCAGCTATTTAAGGGGAGCAGGAGTGAGAACAAACAGAC 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1165 CCCTGCAGAGGGAAGAGCTATTTAAGGGCAGTTGGAATTCAGGAAAAACAAGAC 1218
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 13
US-09-808-388-3
; Sequence 3, Application US/09808388
; Patent No. US20020081719A1
; GENERAL INFORMATION:
; APPLICANT: Massaad, Charbel
; APPLICANT: Berenbaum, Francis
; APPLICANT: Olivier, Jean-Luc
; APPLICANT: Salvat, Collette
; APPLICANT: Bereziat, Gilbert
; TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising them
; FILE REFERENCE: ST00010
; CURRENT APPLICATION NUMBER: US/09/808,388
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: FR/00/03262
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/196,959
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PPRE element
US-09-808-388-3

Query Match 12.3%; Score 41; DB 9; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CAAACTAGTCAAAGGTATCAAACTAGGTCAAAGGTCA 53
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 CAAAACTAGTCAAAGGTATCAAACTAGGTCAAAGGTCA 41
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
US-10-387-495-8/c
; Sequence 8, Application US/10387495
; Publication No. US20030162956A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Leukocyte Regulatory Factors 1 and 2
; FILE REFERENCE: PF359C1
; CURRENT APPLICATION NUMBER: US/10/387,495
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: US/09/603,735A
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 09/055,998
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 60/043,483
; PRIOR FILING DATE: 1997-04-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 371
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-10-387-495-8

Query Match 10.3%; Score 34.2; DB 15; Length 371;
Best Local Similarity 51.7%; Pred. No. 0.24;
Matches 78; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 84 TGTTTTGGCATCAGCTACTGACACGTAAGGTTTCCCAATCCTCAACTCTCTCTGCCGAGC 143
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 238 TGTGTGGGAACAGCCGCCAGGTCAGTGTAGCTCCCTCAATCCTCCACCC 179
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 144 TGATGAGGGGAAGAAAGGATTACCTAGGGGTATGGGAGCAACAACTCTGAGTCCACCAA 203
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 178 AGCACTCAGAGGGAGGGGAGAGAGGTGTGCCCGGTGTGAGTCTCAGCGGCCTC 119
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 204 CTGACCAAGCCCATCCCCAGCCCTTGTGCCTC 234
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 118 CTGAGCTCGCAGCCACAGGCCTTGTGCCTC 88
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 15
US-10-027-632-151276/c
; Sequence 151276, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108927.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151276
; LENGTH: 742
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-151276

Query Match 10.3%; Score 34.2; DB 13; Length 742;
Best Local Similarity 53.3%; Pred. No. 0.33;
Matches 72; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 117 CCCAATCTCAACTCTGTCTGCCAGCTGATAGGGGAAGGAAGGATTACCTAGGGGT 176
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 489 CCCAAACCCAAAGGAGGCTTAACAGTTGCTGAGAGGGAAGCTGCTCCATAGGGCG 430
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 177 ATGGGGGACCAATCCTGAGTCCACCACTGACCACGCCCATGCCCTTGTGCCTCAC 236
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 429 GTGGGCCCATCGTTTCTCAGTCCCCAAAGAAAGAGGTATGTTCTCCCCACAGCCACA 370
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 237 CTACCCCCAACCTCC 251
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 369 GCATCTCCAACCCCC 355
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Search completed: September 11, 2004, 14:11:18
Job time : 323.028 secs
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OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 08:16:17 ; Search time 52.2049 Seconds
(without alignments)
3529.238 Million cell updates/s

Title: US-09-808-388-6

Perfect score: 332

Sequence: 1 gtaccaattcgacaaaacta.....caactctggagtcctctgag 332

Scoring table: IDENTITY NIC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08.

FOC-processing: Minimum Match 0%
Maximum Match 100%

Maximum MATCH 100%
Listing first 45 summaries

1. The first step is to identify the problem or question that needs to be addressed. This involves understanding the context and the specific requirements of the task.

Database : Issued Patents NA: *

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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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2: /cgn2_6/ptodata/2/ina/5B COMB, seq.*
3: /cgn2_6/ptodata/2/ina/6A COMB, seq.*
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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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5: /cgn2_6/ptodata/2/ina/PCTUS COMB.se

6: /cgn2_6/ptodata/2/ina/backfiles1.se

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	
1	33.8	10.2	420	4	US-09-547-435-17	Sequence 17, Appl	
2	33.8	10.2	1441	4	US-09-547-435-13	Sequence 13, Appl	
3	33.8	10.2	2236	4	US-09-547-435-5	Sequence 5, Appl	
4	33.8	10.2	2604	4	US-09-547-435-23	Sequence 23, Appl	
5	33.8	10.2	2701	4	US-09-547-435-1	Sequence 1, Appl	
6	33.8	10.2	3384	4	US-09-547-435-29	Sequence 29, Appl	
C 7	31.8	9.6	1036	4	US-09-547-435-25	Sequence 25, Appl	
C 8	30.6	9.2	305	3	US-09-205-258-86	Sequence 86, Appl	
C 9	30.6	9.2	2885	4	US-09-328-111-618	Sequence 118, Appl	
10	30.4	9.2	1549	2	US-09-016-434-1143	Sequence 618, Appl	
11	30.2	9.1	340	4	US-08-856-44-1	Sequence 1143, Appl	
12	30.2	9.1	1794	4	US-09-833-381-1715	Sequence 1, Appl	
13	29.6	8.9	9299	3	US-09-620-312D-988	Sequence 1715, Appl	
C 14	29.4	8.9	891	4	US-08-458-434A-7	Sequence 988, Appl	
15	29.2	8.8	3111	2	US-09-711-164-156	Sequence 7, Appl	
C 16	29	8.7	205	4	US-09-014-969-12	Sequence 156, Appl	
C 17	29	8.7	455	4	US-09-506-729-37	Sequence 12, Appl	
C 18	29	8.7	1883	1	US-09-621-976-2670	Sequence 37, Appl	
C 19	29	8.7	1933	1	US-08-202-056-2	Sequence 2670, Appl	
C 20	29	8.7	1933	1	US-08-076-093A-1	Sequence 2, Appl	
C 21	29	8.7	1933	1	US-08-410-451-1	Sequence 1, Appl	
C 22	29	8.7	1933	1	US-08-410-455-1	Sequence 1, Appl	
C 23	29	8.7	1933	1	US-08-418-919-1	Sequence 1, Appl	
C 24	29	8.7	1933	1	US-08-410-453A-2	Sequence 1, Appl	
C 25	29	8.7	1933	1	US-08-701-265-1	Sequence 2, Appl	
C 26	29	8.7	1933	1	US-08-410-454A-2	Sequence 1, Appl	
C 27	29	8.7	1933	2	US-08-284-586-1	Sequence 1, Appl	
		8.7	1933	2	US-08-410-456A-2	Sequence 2, Appl	

C	28	29	8, 7	1933	2	US-08-805-478-1	Sequence 1, Appli
C	29	29	8, 7	1933	2	US-08-802-627A-1	Sequence 1, Appli
C	30	29	8, 7	1933	2	US-08-801-238-1	Sequence 1, Appli
C	31	29	8, 7	1933	2	US-08-801-228-1	Sequence 1, Appli
C	32	29	8, 7	1933	3	US-09-104-296-1	Sequence 1, Appli
C	33	29	8, 7	1933	4	US-09-023-655-1134	Sequence 1134, Ap
C	34	29	8, 7	1933	5	PCT-US94-06380-1	Sequence 1, Appli
C	35	28, 8	8, 7	231	4	US-09-023-655-321	Sequence 321, App
C	36	28, 8	8, 7	663	4	US-09-107-532A-2422	Sequence 2422, Ap
C	37	28, 6	8, 6	3728	1	US-08-111-939-1	Sequence 1, Appli
C	38	28, 4	8, 6	501	4	US-09-252-991A-1891	Sequence 1891, Ap
C	39	28, 4	8, 6	666	4	US-09-282-991A-2156	Sequence 2156, Ap
C	40	28, 4	8, 6	708	4	US-09-282-991A-1729	Sequence 1729, Ap
C	41	28, 4	8, 6	897	4	US-09-282-991A-2083	Sequence 2083, Ap
C	42	28, 4	8, 6	1119	4	US-09-252-991A-1806	Sequence 1806, Ap
C	43	28, 4	8, 6	2992	4	US-09-362-123A-3	Sequence 3, Appli
C	44	28, 4	8, 6	9053	4	US-09-976-594-306	Sequence 306, App
C	45	28, 2	8, 5	333	1	US-08-186-895-3	Sequence 4, Appli

ALIGNMENTS

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RESULT 1
US-09-547-435-17
; Sequence 17, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxxygenase Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-547-435-17

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Query Match	10.2%;	Score 33.8;	DB 4;	Length 420;
Best Local Similarity	53.4%;	Pred. No. 0.061;		
Matches	71;	Conservative	0;	Mismatches 62; Indels 0; Gaps 0
129	CTCTGTCCTGCCAGCTGATGAGGGGAAGGAAGGGATTACCTAGGGGTATGGGACCAA	188		
bb				
36	CTCTGCCACGACGCTGCTGTCAACAGTGGGAGCATGACTTTGGGGCTCGATGCCAA	95		
yy				
189	TCTGAGTCCACCACTGACACCGCCCTCCCGACCTTGTGCCTCACTACCCCCCAACC	248		
bb				
96	TGCTCATCATCCATGAGGCAGCCCCCAGACCAAGGGGACCAACCTGAAAGAC	155		
yy				
249	TCCGAGGGGAGC	261		
bb				
156	TTACCTAGACACC	168		
yy				

RESULT 2
US-09-547-435-13
; Sequence 13, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.

```

; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 1441
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-547-435-13

Query Match      10.2%; Score 33.8; DB 4; Length 1441;
Best Local Similarity 53.4%; Pred. No. 0.12;
Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 129 CTCTGCTCTGCCAGCTGATGAGGGGAGGAAAGGATTACCTAGGGGTATGGCGACCAA 188
Db 492 CTCTGCCAGCAGCGTGTCTCAACAGTGGGAGCATGACTTTGGGGCTGGATGCCCAA 551
QY 189 TCCTGAGTCCCACTGACCAAGCCCATCCAGCCTTGTGCTCACTACCCCAACC 248
Db 552 TGCTCCATCATTCATGAGGAGCCCCACCCAGACCAAGGGGACCACCCCTGAAGAC 611
QY 249 TCCCAGAGGGAGC 261
Db 612 TTACCTAGACACC 624

RESULT 3
US-09-547-435-5
; Sequence 5, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2236
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-547-435-5

Query Match      10.2%; Score 33.8; DB 4; Length 2236;
Best Local Similarity 53.4%; Pred. No. 0.15;
Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 129 CTCTGCTCTGCCAGCTGATGAGGGGAGGAAAGGATTACCTAGGGGTATGGCGACCAA 188
Db 1287 CTCTGCCAGCAGCGTGTCTCAACAGTGGGAGCATGACTTTGGGGCTGGATGCCCAA 1346
QY 189 TCCTGAGTCCCACTGACCAAGCCCATCCAGCCTTGTGCTCACTACCCCAACC 248
Db 1347 TGCTCCATCATTCATGAGGAGCCCCACCCAGACCAAGGGGACCACCCCTGAAGAC 1406
QY 249 TCCCAGAGGGAGC 261
Db 1407 TTACCTAGACACC 1419

RESULT 4
US-09-547-435-23
; Sequence 23, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 1441
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-547-435-23

Query Match      10.2%; Score 33.8; DB 4; Length 1441;
Best Local Similarity 53.4%; Pred. No. 0.12;
Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 129 CTCTGCTCTGCCAGCTGATGAGGGGAGGAAAGGATTACCTAGGGGTATGGCGACCAA 188
Db 492 CTCTGCCAGCAGCGTGTCTCAACAGTGGGAGCATGACTTTGGGGCTGGATGCCCAA 551
QY 189 TCCTGAGTCCCACTGACCAAGCCCATCCAGCCTTGTGCTCACTACCCCAACC 248
Db 552 TGCTCCATCATTCATGAGGAGCCCCACCCAGACCAAGGGGACCACCCCTGAAGAC 611
QY 249 TCCCAGAGGGAGC 261
Db 612 TTACCTAGACACC 624

RESULT 5
US-09-547-435-1
; Sequence 1, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2701
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-547-435-1

Query Match      10.2%; Score 33.8; DB 4; Length 2701;
Best Local Similarity 53.4%; Pred. No. 0.16;
Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 129 CTCTGCTCTGCCAGCTGATGAGGGGAGGAAAGGATTACCTAGGGGTATGGCGACCAA 188
Db 1752 CTCTGCCAGCAGCGTGTCTCAACAGTGGGAGCATGACTTTGGGGCTGGATGCCCAA 1811
QY 189 TCCTGAGTCCCACTGACCAAGCCCATCCAGCCTTGTGCTCACTACCCCAACC 248
Db 1812 TGCTCCATCATTCATGAGGAGCCCCACCCAGACCAAGGGGACCACCCCTGAAGAC 1871
QY 249 TCCCAGAGGGAGC 261
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; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 1441
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-547-435-13

Query Match      10.2%; Score 33.8; DB 4; Length 1441;
Best Local Similarity 53.4%; Pred. No. 0.12;
Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 129 CTCTGCTCTGCCAGCTGATGAGGGGAGGAAAGGATTACCTAGGGGTATGGCGACCAA 188
Db 492 CTCTGCCAGCAGCGTGTCTCAACAGTGGGAGCATGACTTTGGGGCTGGATGCCCAA 551
QY 189 TCCTGAGTCCCACTGACCAAGCCCATCCAGCCTTGTGCTCACTACCCCAACC 248
Db 552 TGCTCCATCATTCATGAGGAGCCCCACCCAGACCAAGGGGACCACCCCTGAAGAC 611
QY 249 TCCCAGAGGGAGC 261
Db 612 TTACCTAGACACC 624

RESULT 3
US-09-547-435-5
; Sequence 5, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2236
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-547-435-5

Query Match      10.2%; Score 33.8; DB 4; Length 2236;
Best Local Similarity 53.4%; Pred. No. 0.15;
Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 129 CTCTGCTCTGCCAGCTGATGAGGGGAGGAAAGGATTACCTAGGGGTATGGCGACCAA 188
Db 1287 CTCTGCCAGCAGCGTGTCTCAACAGTGGGAGCATGACTTTGGGGCTGGATGCCCAA 1346
QY 189 TCCTGAGTCCCACTGACCAAGCCCATCCAGCCTTGTGCTCACTACCCCAACC 248
Db 1347 TGCTCCATCATTCATGAGGAGCCCCACCCAGACCAAGGGGACCACCCCTGAAGAC 1406
QY 249 TCCCAGAGGGAGC 261
Db 1407 TTACCTAGACACC 1419

RESULT 4
US-09-547-435-23
; Sequence 23, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 1441
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-547-435-23

Query Match      10.2%; Score 33.8; DB 4; Length 1441;
Best Local Similarity 53.4%; Pred. No. 0.12;
Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 129 CTCTGCTCTGCCAGCTGATGAGGGGAGGAAAGGATTACCTAGGGGTATGGCGACCAA 188
Db 492 CTCTGCCAGCAGCGTGTCTCAACAGTGGGAGCATGACTTTGGGGCTGGATGCCCAA 551
QY 189 TCCTGAGTCCCACTGACCAAGCCCATCCAGCCTTGTGCTCACTACCCCAACC 248
Db 552 TGCTCCATCATTCATGAGGAGCCCCACCCAGACCAAGGGGACCACCCCTGAAGAC 611
QY 249 TCCCAGAGGGAGC 261
Db 612 TTACCTAGACACC 624

RESULT 5
US-09-547-435-1
; Sequence 1, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2701
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-547-435-1

Query Match      10.2%; Score 33.8; DB 4; Length 2701;
Best Local Similarity 53.4%; Pred. No. 0.16;
Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 129 CTCTGCTCTGCCAGCTGATGAGGGGAGGAAAGGATTACCTAGGGGTATGGCGACCAA 188
Db 1752 CTCTGCCAGCAGCGTGTCTCAACAGTGGGAGCATGACTTTGGGGCTGGATGCCCAA 1811
QY 189 TCCTGAGTCCCACTGACCAAGCCCATCCAGCCTTGTGCTCACTACCCCAACC 248
Db 1812 TGCTCCATCATTCATGAGGAGCCCCACCCAGACCAAGGGGACCACCCCTGAAGAC 1871
QY 249 TCCCAGAGGGAGC 261
```

[illegible]

LOCATION: (1024)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (1032)
OTHER INFORMATION: n equals a,t,g, or c
US-09-205-258-86

Query Match
Best Local Similarity 9.6%; Score 31.8; DB 4; Length 1036;
Matches 69; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 189 TCTGTGAGTCACCACTGACACGCCCATCCCGAGCTTGTGCTCCTACCTACCCCAACC 248
|||||
Db 852 TCTGTGCTCTCCACGCCCTGCCAGCCCTTCTGTGCTCTCCCGGCCCGCCAGGC 793
|||||

QY 249 TCCGAGGAGGAGCTATTAAAGGGGAGCAGAGTGCAGAACAAACAGAGCGCTGGG 308
|||||
Db 792 CAGCGCTGGCCAGCAATGCAATGCTGGGGTGGGATCACCAAGAGAGGCCAAGC 733
|||||

QY 309 GATACACTCT 319
Db 732 CAACTACCCCT 722

RESULT 8
US-09-328-111-618/c
Sequence 618, Application US/09328111
Patent No. 6262333
GENERAL INFORMATION:
APPLICANT: Endege, Wilson O.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Astle, Jon H.
APPLICANT: Burgess, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
APPLICANT: Catino, Theodore J.
APPLICANT: Derti, Adnan
APPLICANT: Ford, Donna M.
APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 618
LENGTH: 305
TYPE: DNA
ORGANISM: Homo sapiens
US-09-328-111-618

Query Match
Best Local Similarity 9.2%; Score 30.6; DB 3; Length 305;
Matches 57; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 64 CGGCAAACTGCTGAAATGTGTTTGGCATCAGCTACTGACACGTAAGGTTTCCCAATC 123
|||||
Db 217 CGCCAAATAAACACGATGTTGTGTAAACATCCCCCAGTGGGGCTAGAAATTCCTCATG 158
|||||

QY 124 CTCACCTGTCTGCCAGCTGATGAGGGGAAGGAAGGA 164
Db 157 GTGACCTGTGACCTGCTCCCTGAGACAGGGGAGCCAGGCA 117
|||||

RESULT 9
US-09-016-434-1143/c
Sequence 1143, Application US/09016434

Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1143:
SEQUENCE CHARACTERISTICS:
LENGTH: 2885 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g1478280
US-09-016-434-1143

Query Match
Best Local Similarity 9.2%; Score 30.6; DB 4; Length 2885;
Matches 57; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 64 CGGCAAACTGCTGAAATGTGTTTGGCATCAGCTACTGACACGTAAGGTTTCCCAATC 123
Db 2633 CGCCAAATAAACACGATGTTGTGTAAACATCCCCCAGTGGGGCTAGAAATTCCTCATG 2574
|||||

QY 124 CTCACCTGTCTGCCAGCTGATGAGGGGAAGGAAGGA 164
Db 2573 GTGACCTGTGACCTGCTCCCTGAGACAGGGGAGCCAGGCA 2533
|||||

RESULT 10
US-08-856-444-1
Sequence 1, Application US/08856444
Patent No. 5959081
GENERAL INFORMATION:
APPLICANT: Lecka-Czernik, Beata
TITLE OF INVENTION: No. 5959081el Zinc Binding LIM Protein S2-6
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benjamin Aaron Adler, Ph.D. J.D.
STREET: 8011 Candle Lane
CITY: Houston
STATE: Texas
ZIP: 77071
COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 Mb floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,444
FILING DATE: May 14, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5988
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
TELEFAX: (713) 777-6908
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1549 bp

TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: c-DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:

US-08-856-444-1

Query Match 9.2%; Score 30.4; DB 2; Length 1549;
Best Local Similarity 57.3%; Pred. No. 1.8;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 111 AGTTTCCCAATCCTCAACTCTGTCTGCCAGCTGATGAGGGAAGGAAGGATTACCT 170
DB 530 AAGTGGCCCTCCGGCAGGCTGTGCTGCCAAGGAGGAGGGAAGCAGCAGGAAGCC 589
QY 171 AGGGGTATGGCGACCAATCCTGATCCCAACTG 206
DB 590 AGAGGGGCGAGAGCACTGCTGTACCACCAACGG 625

RESULT 11
US-09-833-381-1715
Sequence 1715, Application US/09833381
Patent No. 6672186
GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1715
LENGTH: 340
TYPE: DNA
ORGANISM: Homo sapiens
US-09-833-381-1715

Query Match 9.1%; Score 30.2; DB 4; Length 340;
Best Local Similarity 62.7%; Pred. No. 0.96;
Matches 47; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 132 TGTCCTCCAGCTGATGAGGGGAAGGAAGGATTACTAGGGGTATGGGCGACCAATCC 191
DB 72 TGGCTTGCCCAAGGAGGAGGGGAAGCAGCAGAAAGCCAGAGGGGCGAGAGCACTGC 131
QY 192 TGAGTCCACCAACTG 206
DB 132 TGCTACCACCAACGG 146

RESULT 12
US-09-620-312D-988
Sequence 988, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yunqing
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Dmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt FL_genes Version 1.0
SEQ ID NO 988
LENGTH: 1794
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (164)..(1261)
US-09-620-312D-988

Query Match 9.1%; Score 30.2; DB 4; Length 1794;
Best Local Similarity 62.7%; Pred. No. 2.3;
Matches 47; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 132 TGTCCTCCAGCTGATGAGGGGAAGGAAGGATTACTAGGGGTATGGGCGACCAATCC 191
DB 778 TGGCTTGCCCAAGGAGGAGGGGAAGCAGCAGAAAGCCAGAGGGGCGAGAGCACTGC 837
QY 192 TGAGTCCACCAACTG 206
DB 838 TGCTACCACCAACGG 852

RESULT 13
US-08-458-434A-7/c
Sequence 7, Application US/08458434A
Patent No. 6083690
GENERAL INFORMATION:
APPLICANT: Harris Ph.D., Stephen E.
APPLICANT: Mundy M.D., Gregory R.
APPLICANT: Gosh-Choudhury Ph.D., Nandini
APPLICANT: Feng Ph.D., Jian Q.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING

TITLE OF INVENTION: OSTEOGENIC AGENTS

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: James C. Weseman, Esq.

STREET: 401 B. Street, Suite 1700

CITY: San Diego

STATE: CA

COUNTRY: USA

ZIP: 92101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/458,434A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Weseman, James C.

REGISTRATION NUMBER: 30,507

REFERENCE/DOCKET NUMBER: P00060US0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 699-3604

TELEFAX: 619-236-1048

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 9299 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-458-434A-7

Query Match 8.9%; Score 29.6; DB 3; Length 9299;

Best Local Similarity 59.5%; Pred. No. 9.1;

Matches 50; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 211 CGCCCATCCCGAGCTTGTGCTACCTACCCCACTCCAGAGGAGGAGCTATTATTA 270

Db 6318 CCCCCCACC CGCGCTTCTCGGCTCCAGCCCAATTCACAACTTCAGCTGGTTA 6259

QY 271 AGGGAGGAGGAGTCTCAGACAAA 294

Db 6258 AGAACAGGAGGAGGAGACAGA 6235

RESULT 14

US-09-711-164-156

Sequence 156, Application US/09711164

Patent No. 6589738

GENERAL INFORMATION:

APPLICANT: Forsyth, R. Allyn

APPLICANT: Ohlsen, Kari

APPLICANT: Zyskind, Judith

TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THEREOF

FILE REFERENCE: ELITRA.008A

CURRENT APPLICATION NUMBER: US/09/711,164

CURRENT FILING DATE: 2000-11-09

PRIOR APPLICATION NUMBER: US 60/164415

PRIOR FILING DATE: 1999-11-9

NUMBER OF SEQ ID NOS: 469

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 156

LENGTH: 891

TYPE: DNA

ORGANISM: Escherichia coli

FEATURE:

NAME/KEY: CDS

LOCATION: (1)... (891)

US-09-711-164-156

Query Match

Best Local Similarity 56.8%; Pred. No. 3;

Matches 54; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 52 CAAATTCGACGCGGCAAACTGCCTGAAATGTGTTTGGCATCAGCTACTGACACGTA 111

Db 751 CAATACCTCAACCGCAAACTACCTGTGGGGTGACITTCGCGCGCTGCGGTGATGTCT 810

QY 112 GGTTCGCAATCTCAACTCTGTCTGCCAGCTGA 146

Db 811 GCATTACGATCACCATCGTCTTCTTGTGCTCA 845

RESULT 15

US-09-014-969-12

Sequence 12, Application US/09014969

Patent No. 5965397

GENERAL INFORMATION:

APPLICANT: Jacobs, Kenneth

APPLICANT: McCoy, John M.

APPLICANT: LaVallie, Edward R.

APPLICANT: Racie, Lisa A.

APPLICANT: Merberg, David

APPLICANT: Treacy, Maurice

APPLICANT: Spaulding, Vikki

APPLICANT: Agostino, Michael J.

TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 CambridgePark Drive

CITY: Cambridge

STATE: MA

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/014,969

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Sprunger, Suzanne A.

REGISTRATION NUMBER: 41,323

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8284

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 3111 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-09-014-969-12

Query Match

Best Local Similarity 57.8%; Pred. No. 7;

Matches 52; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 133 GTCCTGCCAGCTGATCAGGGGAGGAAAGGATTACCTAGGGGTATGGCGACCAATCCT 192

Db 957 GTCGTCCCGGCTGATCAGCAGCTTGAGATAGAAAGACTACAGGTGAGCTGTCCAAATCC 1016

QY 193 GAGTCCACCACTGACACGCGCCATCCCA 222

Db 1017 CATGCGGGATCTTCCACACCCGCTCTCA 1046

Search completed: September 11, 2004, 09:33:15
Job time : 52.2049 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 09:20:47 ; Search time 262.86 Seconds
(without alignments)
5187.326 Million cell updates/sec

Title: US-09-808-388-5

Perfect score: 271

Sequence: 1 cgcggcaaaactgctgaaa.....caactctggagctctctgag 271

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 6608766

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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2	271	100.0	332	9	US-09-808-388-6
3	212	78.2	1080	10	US-09-865-866-17
4	164.2	60.6	6083	13	US-10-221-714A-440
5	150.2	55.4	6083	13	US-10-221-714A-439
6	118.8	43.8	967	15	US-10-210-120-75
7	84.4	31.1	3330	9	US-09-917-800A-1495
8	84.4	31.1	3330	12	US-10-152-319A-2157
9	84.4	31.1	3330	16	US-10-191-803-398
10	80.8	29.8	1076	9	US-09-925-300-70
11	50	18.5	735	9	US-09-981-353-17
12	49.6	18.3	4990	10	US-09-865-866-97
13	34.2	12.6	371	15	US-10-387-495-8
14	34.2	12.6	742	13	US-10-027-632-151276

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	17	33.8	12.5	1441	15	US-10-422-264-13
	18	33.8	12.5	2136	9	US-09-862-658-3
	19	33.8	12.5	2136	15	US-10-175-596-24
	20	33.8	12.5	2136	17	US-10-776-871-24
	21	33.8	12.5	2236	15	US-10-422-264-5
	22	33.8	12.5	2307	13	US-10-302-172-803
	23	33.8	12.5	2604	15	US-10-422-264-23
	24	33.8	12.5	2701	15	US-10-422-264-1
	25	33.8	12.5	3320	9	US-09-862-658-1
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	27	33.8	12.5	3320	17	US-10-776-871-22
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	30	32.6	12.0	54552	13	US-10-087-192-1303
c	31	32.4	12.0	819	13	US-10-027-632-130312
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	34	32.2	11.9	573	13	US-10-027-632-50048
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	37	32.2	11.9	573	13	US-10-027-632-69880
	38	32.2	11.9	573	13	US-10-027-632-69881
	39	32.2	11.9	573	13	US-10-027-632-70565
	40	32.2	11.9	573	13	US-10-027-632-70566
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	43	32.2	11.9	573	16	US-10-027-632-69880
	44	32.2	11.9	573	16	US-10-027-632-69881
	45	32.2	11.9	573	16	US-10-027-632-70565

ALIGNMENTS

RESULT 1
US-09-808-388-5
; Sequence 5, Application US/09/808,388
; Patent No. US2002008179A1
; GENERAL INFORMATION:
; APPLICANT: Massaad, Charbel
; APPLICANT: Berenbaum, Francis
; APPLICANT: Olivier, Jean-Luc
; APPLICANT: Salvat, Colette
; APPLICANT: Berezat, Gilbert
; TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising them
; TITLE OF INVENTION: their uses
; FILE REFERENCE: ST00010
; CURRENT APPLICATION NUMBER: US/09/808,388
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: FR/00/03262
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/196,959
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 5
; LENGTH: 271
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fragment of the PLA2s promoter
US-09-808-388-5

Query Match 100.0%; Score 271; DB 9; Length 271;
Best Local Similarity 100.0%; Pred. No. 1.5e-85;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCAAACTGCCTGAATCTGTTTGGCATCAGTACTGACGTAAGTTTCCCAA 60

Db 1 CGCGCAAACTGCCTGAATCTGTTTGGCATCAGTACTGACGTAAGTTTCCCAA 60

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QY 61 TCCTCAACTCTGCTCCAGCTGATGAGGGGAAGAAAGGGATTACCTAGGGGTATGGG 120
Db 61 TCCTCAACTCTGCTCCAGCTGATGAGGGGAAGAAAGGGATTACCTAGGGGTATGGG 120
QY 121 CGACCAATCTCTGAGTCCACCACTGACCAAGCCCATCCAGCCCTTGGCTTCCCTCACCTACC 180
Db 121 CGACCAATCTCTGAGTCCACCACTGACCAAGCCCATCCAGCCCTTGGCTTCCCTCACCTACC 180
QY 181 CCCAACCTCCAGAGGAGCAGCTATTATTAAGGGAGCAGGAGTGCAGAACAAACAAGACG 240
Db 181 CCCAACCTCCAGAGGAGCAGCTATTATTAAGGGAGCAGGAGTGCAGAACAAACAAGACG 240
QY 241 GCCTGGGGATACAACTCTGGAGTCTCTGAG 271
Db 241 GCCTGGGGATACAACTCTGGAGTCTCTGAG 271

RESULT 2
US-09-808-388-6
; Sequence 6, Application US/09808388
; Patent No. US20020081719A1
; GENERAL INFORMATION:
; APPLICANT: Massead, Charbel
; APPLICANT: Berendaum, Francis
; APPLICANT: Olivier, Jean-Luc
; APPLICANT: Salvat, Collette
; APPLICANT: Bereziat, Gilbert
; TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising them
; FILE REFERENCE: ST00010
; CURRENT APPLICATION NUMBER: US/09/808,388
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: FR/00/03262
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/196,959
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 332
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PPRE/PLA2s hybrid promoter
US-09-808-388-6

Query Match 100.0%; Score 271; DB 9; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.6e-85;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGCGGCAAAACTGCCTGAAATGTTTTGGCATCAGTACGTACGACGTAGGTTTCCCAA 60
Db 62 CGCGGCAAAACTGCCTGAAATGTTTTGGCATCAGTACGTACGACGTAGGTTTCCCAA 121
QY 61 TCCTCAACTCTGCTCCAGCTGATGAGGGGAAGAAAGGGATTACCTAGGGGTATGGG 120
Db 122 TCCTCAACTCTGCTCCAGCTGATGAGGGGAAGAAAGGGATTACCTAGGGGTATGGG 181
QY 121 CGACCAATCTCTGAGTCCACCACTGACCAAGCCCATCCAGCCCTTGGCTTCCCTCACCTACC 180
Db 182 CGACCAATCTCTGAGTCCACCACTGACCAAGCCCATCCAGCCCTTGGCTTCCCTCACCTACC 241
QY 181 CCCAACCTCCAGAGGAGCAGCTATTATTAAGGGAGCAGGAGTGCAGAACAAACAAGACG 240
Db 242 CCCAACCTCCAGAGGAGCAGCTATTATTAAGGGAGCAGGAGTGCAGAACAAACAAGACG 301
QY 241 GCCTGGGGATACAACTCTGGAGTCTCTGAG 271
Db 302 GCCTGGGGATACAACTCTGGAGTCTCTGAG 332

RESULT 3
US-09-865-866-17
; Sequence 17, Application US/09865866
; Publication No. US20030045487A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EXPRESSION
; FILE REFERENCE: RTS-0221
; CURRENT APPLICATION NUMBER: US/09/865,866
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 17
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-865-866-17

Query Match 78.2%; Score 212; DB 10; Length 1080;
Best Local Similarity 93.1%; Pred. No. 1.9e-64;
Matches 255; Conservative 0; Mismatches 15; Indels 4; Gaps 3;
QY 1 CGCGGCAAAACTGCCTGAAATGTTTTGGCATCAGTACGTACGACGATAA-CGTTTCCCA 59
Db 763 CTGCGCAAAACTGCCTGAAATGTTTTGGCATCAGTACGTACGACGATAAAGGTTTCCCA 822
QY 60 ATCCTCAACTCTGCTCTG-CCAGCTGATGAGGGGAAGAAAGGGATTACCTAGGGGTAT 117
Db 823 ATCCTCAACTCTGCTCTGCTGCCAGGCTGATGAGGGGAAGAAAGGGATTACCTAGGGGTAT 882
QY 118 GGGCGACCAATCCTGAGTCCACCACTGACACCGCCCATCCCGAGCTTGTGCTCACCT 177
Db 883 GGGCGACCAATCCTGAGTCCACCACTGACACCGCCCATCCCGAGCTTGTGCTCACCT 942
QY 178 ACCCCCACTCCAGAGGAGCAGCTATTATTAAGGGAGCAGGAGTGCAGAACAAACAAG 237
Db 943 ACCCCCACTCCAGAGGAGCAGCTATTATTAAGGGAGCAGGAGTGCAGAACAAACAAG 1001
QY 238 ACGGCTGGGGATACAACTCTGGAGTCTCTGAG 271
Db 1002 ACGGCTGGGGATACAACTCTGGAGTCTCTGAG 1035

RESULT 4
US-10-221-714A-440/c
; Sequence 440, Application US/10221714A
; Publication No. US20040048254A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with tumor suppressor genes and oncogenes
; FILE REFERENCE: 5013.1005
; CURRENT APPLICATION NUMBER: US/10/221,714A
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: PCT/EP01/02955
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: DE 10013847.0
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 540
; SEQ ID NO 440
; LENGTH: 6083
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1495
; LENGTH: 3330
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 X51529
US-09-917-800A-1495

Query Match 31.1%; Score 84.4; DB 9; Length 3330;
Best Local Similarity 64.9%; Pred. No. 4.4e-19;
Matches 157; Conservative 0; Mismatches 81; Indels 4; Gaps 2;

QY 6 CAAACTGCCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAATCCTC 65
DB 260 CCAATCAGCTAAAGTTTATGATGCGCACACCCATGGTATGAGGGCTTTTCCGCCCCC 319

QY 66 AACTCTGTCTGCCAGCTGATGAGGGGAAGAAAGGATTACCTAGGGGTATGGG - CGA 123
DB 320 AAGCTGTCTGCCAGCTGTTGGGGGAAAGGGGAAATACCCAGGGGGTGGGTATGC 379

QY 124 CCAATCTGTGCTGCCAGCTGATGAGGGGAAGAAAGGATTACCTAGGGGTATGGG - CGA 181
DB 380 CGCTGTGTAATCCATTATTTGGCCACACCCACCTCCCATCTCCCTGTGGCTCTCCGATCC 439

QY 182 CCAACTCTCCAGAGGAGCAGCTATTTAAGGGGAGCAGAGTGCGAGAACAAACAAGACGG 241
DB 440 CCAGCCCTGCAGAGGGAAGAGCTATTTAAGAGCATTTGGAGTACAGGAAACAGGCAG 499

QY 242 CC 243
DB 500 GC 501

RESULT 8
US-10-152-319A-2157
; Sequence 2157, Application US/10152319A
; Publication No. US20040072160A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Higgs, Brandon
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 4921-5099-US
; CURRENT APPLICATION NUMBER: US/10/152,319A
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/292,335
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/297,523
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,925
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,810
; PRIOR FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: US 60/303,807
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,808
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/315,047
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: US 60/324,928
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/330,867
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/330,462
; PRIOR FILING DATE: 2001-10-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2221
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2157
; LENGTH: 3330
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. X51529
US-10-152-319A-2157

Query Match 31.1%; Score 84.4; DB 12; Length 3330;
Best Local Similarity 64.9%; Pred. No. 4.4e-19;
Matches 157; Conservative 0; Mismatches 81; Indels 4; Gaps 2;

QY 6 CAAACTGCCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAATCCTC 65
DB 260 CCAATCAGCTAAAGTTTATGATGCGCACACCCATGGTATGAGGGCTTTTCCGCCCCC 319

QY 66 AACTCTGTCTGCCAGCTGATGAGGGGAAGAAAGGATTACCTAGGGGTATGGG - CGA 123
DB 320 AAGCTGTCTGCCAGCTGTTGGGGGAAAGGGGAAATACCCAGGGGGTGGGTATGC 379

QY 124 CCAATCTGTGCTGCCAGCTGATGAGGGGAAGAAAGGATTACCTAGGGGTATGGG - CGA 181
DB 380 CGCTGTGTAATCCATTATTTGGCCACACCCACCTCCCATCTCCCTGTGGCTCTCCGATCC 439

QY 182 CCAACTCTCCAGAGGAGCAGCTATTTAAGGGGAGCAGAGTGCGAGAACAAACAAGACGG 241
DB 440 CCAGCCCTGCAGAGGGAAGAGCTATTTAAGAGCATTTGGAGTACAGGAAACAGGCAG 499

QY 242 CC 243
DB 500 GC 501

RESULT 9
US-10-191-803-398
; Sequence 398, Application US/10191803
; Publication No. US20040014040A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Higgs, Brandon
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
; FILE REFERENCE: 4921-5090US
; CURRENT APPLICATION NUMBER: US/10/191,803
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/303,819
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/305,623
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/369,351
; PRIOR FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: US 60/377,611
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 1140
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 398
; LENGTH: 3330
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20040014040A1 X51529
US-10-191-803-398

Query Match      31.1%; Score 84.4; DB 16; Length 3330;
Best Local Similarity 64.9%; Pred. No. 4.4e-19;
Matches 157; Conservative 0; Mismatches 81; Indels 4; Gaps 2;

QY      6 CAAACTGCTGAAATGCTGTTTGGCATCAGCTACTGACACGTAAGGTTTCCCAATCCTC 65
Db      260 CGAAATCAGCTAAAGTTTATGATGGCCACAAACCCATGATGAGGGCTTTTCCGGGCCCTC 319

QY      66 AACTCTGTCTGCTGCAGCTGATGAGGGGAAGAAAGGATTACCTAGGGGTATGG--CGA 123
Db      320 AAGGCTGTTCTGCCAGCTGTTGGGGGAAAGGGGAATTTACCCAGGGCGTTGGGTATGC 379

QY      124 CCAATCTGAGTCCAACTGACACCGCCCA--TCCCCAGCCTTGTGCTCCTACCTACCC 181
Db      380 CCGTCTGTGAATCCATTATTATTGGCCACACCCACCTCCCATCCCTGTGGCTCTCCGATCC 439

QY      182 CCACCTCCAGAGGAGCAGCTATTTAAGGGAGCAGGAGTGCAGAACAAACAGACGG 241
Db      440 CCAGCCTCGCAGAGGGAAGAGCTATTTAAGAGCATTGGGAGTACAGGAAAAACAGGCAG 499

QY      242 CC 243
Db      500 GC 501

RESULT 10
US-09-925-300-70
; Sequence 70, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 70
; LENGTH: 1076
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (911)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-70

Query Match      29.8%; Score 80.8; DB 9; Length 1076;
Best Local Similarity 95.3%; Pred. No. 5.8e-18;
Matches 82; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      186 CTTCCAGAGGAGCAGCTATTTAAGGGAGCAGGAGTGCAGAACAAACAGAGCGGCTG 245
Db      2 CCAACAGAGGAGCAGCTATTTAAGGGAGCAGGAGTGCAGAACAAACAGAGCGGCTG 61

QY      246 GGGATACAACTCTGGAGTCTCTGAG 271
Db      62 GGGATACAACTCTGGAGTCTCTGAG 87
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RESULT 11
US-09-981-353-17
; Sequence 17, Application US/09981353
; Patent No. US20020160382A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; APPLICANT: Jones, David A.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 17
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 474322.36
; NAME/KEY: unsure
; LOCATION: 388
; OTHER INFORMATION: a, t, c, g, or other
US-09-981-353-17

Query Match      18.5%; Score 50; DB 9; Length 735;
Best Local Similarity 100.0%; Pred. No. 4.2e-07;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      222 GTGCAGAACAAACAGACGGCCTGGGATACAACTCTGGAGTCTCTGAG 271
Db      1 GTGCAGAACAAACAGACGGCCTGGGATACAACTCTGGAGTCTCTGAG 50

RESULT 12
US-09-865-866-97
; Sequence 97, Application US/09865866
; Publication No. US20030045487A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EXH
; FILE REFERENCE: RTS-0221
; CURRENT APPLICATION NUMBER: US/09/865,866
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 97
; LENGTH: 4990
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2026)...(2068)
; NAME/KEY: CDS
; LOCATION: (2245)...(2389)
; NAME/KEY: CDS
; LOCATION: (2622)...(2731)
; NAME/KEY: CDS
; LOCATION: (4098)...(4240)
US-09-865-866-97

Query Match      18.3%; Score 49.6; DB 10; Length 4990;
Best Local Similarity 59.4%; Pred. No. 1.1e-06;
Matches 139; Conservative 0; Mismatches 64; Indels 31; Gaps 2;

QY      6 CAAACTGCTGAAATGCTGTTTGGCATCAGCTACTGACACGTAAGGTTTCCCAATCCTC 65
Db      1016 CAAATCAGCTGAAATTTATGATGGCGCACCCCTTGGTATGAGGCTTTTCCAGCCCTC 1075

QY      66 AACTCTGTCTGCCAGCTGATGAGGGGAAGAAAGGATTACCTAGGGGTATGGGCGACC 125
Db      1076 AGGGCTGCCCTGCCAGCTGTTGGGGAACAAAAGGCAATGGGTATGC-----CC 1125
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RESULT 14
US-10-027-632-151276/c
? Sequence 151276, Application US/10027632
? Publication No. US20020198371A1
? GENERAL INFORMATION:
? APPLICANT: Wang, David G.
? TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
? POLYMORPHISMS IN THE HUMAN GENOME
? FILE REFERENCE: 108827.129
? CURRENT APPLICATION NUMBER: US/10/027,632
? CURRENT FILING DATE: 2002-04-30
? PRIOR APPLICATION NUMBER: US 60/218,006
? PRIOR FILING DATE: 2000-07-12
? PRIOR APPLICATION NUMBER: US 60/198,676
? PRIOR FILING DATE: 2000-04-20
? PRIOR APPLICATION NUMBER: US 60/193,483
? PRIOR FILING DATE: 2000-03-29
? PRIOR APPLICATION NUMBER: US 60/185,218
? PRIOR FILING DATE: 2000-02-24
? PRIOR APPLICATION NUMBER: US 60/167,363
? PRIOR FILING DATE: 1999-11-23
? PRIOR APPLICATION NUMBER: US 60/156,358
? PRIOR FILING DATE: 1999-09-28

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[illegible]

Db 369 GCATCTCCAAACCCC 355

Search completed: September 11, 2004, 14:11:17
Job time : 263.86 secs

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Result No.	Score	Query Match	Length	DB	ID	Description
1	33.8	12.5	420	4	US-09-547-435-17	Sequence 17, Appl
2	33.8	12.5	1441	4	US-09-547-435-13	Sequence 13, Appl
3	33.8	12.5	2236	4	US-09-547-435-5	Sequence 5, Appl
4	33.8	12.5	2604	4	US-09-547-435-23	Sequence 23, Appl
5	33.8	12.5	2701	4	US-09-547-435-1	Sequence 1, Appl
6	33.8	12.5	3384	4	US-09-547-435-29	Sequence 29, Appl
C 7	31.8	11.7	1036	4	US-09-205-258-86	Sequence 86, Appl
C 8	30.6	11.3	305	3	US-09-328-111-618	Sequence 618, Appl
C 9	30.6	11.3	2885	4	US-09-016-434-1143	Sequence 1143, Appl
10	30.4	11.2	1549	2	US-08-856-444-1	Sequence 1, Appl
11	30.2	11.1	340	4	US-09-833-381-1715	Sequence 1715, Appl
12	30.2	11.1	1794	4	US-09-620-312D-988	Sequence 988, Appl
C 13	29.6	10.8	9299	3	US-08-458-434A-7	Sequence 7, Appl
C 14	29.2	10.8	3111	2	US-09-014-969-12	Sequence 12, Appl
C 15	29	10.7	204	4	US-09-506-729-37	Sequence 37, Appl
C 16	29	10.7	455	4	US-09-621-976-2670	Sequence 2670, Appl
C 17	29	10.7	1883	1	US-08-202-056-2	Sequence 2, Appl
C 18	29	10.7	1933	1	US-08-076-093A-1	Sequence 1, Appl
C 19	29	10.7	1933	1	US-08-410-451-1	Sequence 1, Appl
C 20	29	10.7	1933	1	US-08-410-455-1	Sequence 1, Appl
C 21	29	10.7	1933	1	US-08-418-919-1	Sequence 1, Appl
C 22	29	10.7	1933	1	US-08-410-453A-2	Sequence 2, Appl
C 23	29	10.7	1933	1	US-08-701-266-1	Sequence 1, Appl
C 24	29	10.7	1933	1	US-08-410-45A-2	Sequence 2, Appl
C 25	29	10.7	1933	2	US-08-284-586-1	Sequence 1, Appl
C 26	29	10.7	1933	2	US-08-410-456A-2	Sequence 2, Appl
C 27	29	10.7	1933	2	US-08-805-478-1	Sequence 1, Appl

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; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 1441
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-547-435-13

Query Match      12.5%; Score 33.8; DB 4; Length 1441;
Best Local Similarity 53.4%; Pred. No. 0.14;
Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy 68 CTCTGTCTGCCAGCTGATGAGGGGAAGGAAGGATTACCTAGGGGTATGGCGACCAA 127
Db 492 CTCTGCCAGACGCTGCTGTCAACAGTGGCAGCATGACTTTGGGGCTGGATGCCCAA 551

Qy 128 TCCTGAGTCCCAACTGACCAACGCCCATCCCCAGCCTTGTGCTCTCACTACCCCAACC 187
Db 552 TGCTCCATCATCCATGAGGAGGCCCAACCCAGACCAAGGGACCACCCCTGAAGAC 611

Qy 188 TCCCAGAGGGAGC 200
Db 612 TTACTAGACACC 624

RESULT 3
US-09-547-435-5
; Sequence 5, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2236
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-547-435-5

Query Match      12.5%; Score 33.8; DB 4; Length 2236;
Best Local Similarity 53.4%; Pred. No. 0.17;
Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy 68 CTCTGTCTGCCAGCTGATGAGGGGAAGGAAGGATTACCTAGGGGTATGGCGACCAA 127
Db 1287 CTCTGCCAGACGCTGCTGTCAACAGTGGCAGCATGACTTTGGGGCTGGATGCCCAA 1346

Qy 128 TCCTGAGTCCCAACTGACCAACGCCCATCCCCAGCCTTGTGCTCTCACTACCCCAACC 187
Db 1347 TGCTCCATCATCCATGAGGAGGCCCAACCCAGACCAAGGGACCACCCCTGAAGAC 1406

Qy 188 TCCCAGAGGGAGC 200
Db 1407 TTACTAGACACC 1419

RESULT 4
US-09-547-435-23
; Sequence 23, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2701
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-547-435-1

Query Match      12.5%; Score 33.8; DB 4; Length 2701;
Best Local Similarity 53.4%; Pred. No. 0.18;
Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy 68 CTCTGTCTGCCAGCTGATGAGGGGAAGGAAGGATTACCTAGGGGTATGGCGACCAA 127
Db 1752 CTCTGCCAGACGCTGCTGTCAACAGTGGCAGCATGACTTTGGGGCTGGATGCCCAA 1811

Qy 128 TCCTGAGTCCCAACTGACCAACGCCCATCCCCAGCCTTGTGCTCTCACTACCCCAACC 187
Db 1812 TGCTCCATCATCCATGAGGAGGCCCAACCCAGACCAAGGGACCACCCCTGAAGAC 1871

Qy 188 TCCCAGAGGGAGC 200
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Db 1872 TTACCTAGACACC 1884

RESULT 6

US-09-547-435-29

; Sequence 29, Application US/09547435

; Patent No. 6582957

; GENERAL INFORMATION:

; APPLICANT: Turner, C. Alexander, Jr.

; APPLICANT: Zambrowicz, Brian

; APPLICANT: Nehls, Michael

; APPLICANT: Friedrich, Glenn

; APPLICANT: Sands, Arthur T.

; TITLE OF INVENTION: No. 6582957el Lipoxxygenase Proteins and Polynucleotides

; FILE OF INVENTION: Encoding the Same

; FILE REFERENCE: 7705.0009-00000

; CURRENT APPLICATION NUMBER: US/09/547,435

; CURRENT FILING DATE: 2000-04-12

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 29

; LENGTH: 3384

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-547-435-29

Query Match 12.5%; Score 33.8; DB 4; Length 3384;

Best Local Similarity 53.4%; Pred. No. 0.2;

Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 68 CTCCTGCTCTGCCAGCTGATCAGGGGGAAGGATTACCTAGGGGTATGGGCGACCAA 127

Db 2250 CTCGCGCCAGCAGCTGCTGTACACATGGGCAGCATGCTTTGGGCGCTGGATGCCCAA 2309

QY 128 TCTGTAGTCACCACTGACACAGCCCATCCCGAGCCCTTGTGCTCACCTACCCCAACC 187

Db 2310 TGTCTCATCATCTCATTGAGGAGCCGCCCAAGGGGACCAACCCCTTGAAGAC 2369

QY 188 TCCACAGGGGAGC 200

Db 2370 TTACCTAGACACC 2382

RESULT 7

US-09-205-258-86/c

; Sequence 86, Application US/09205258

; Patent No. 6525174

; GENERAL INFORMATION:

; APPLICANT: Young et al.

; TITLE OF INVENTION: 207 Human Secreted Proteins

; FILE REFERENCE: PZ007P1

; CURRENT APPLICATION NUMBER: US/09/205,258

; CURRENT FILING DATE: 1998-12-04

; EARLIER APPLICATION NUMBER: PCT/US98/11422

; EARLIER FILING DATE: 1998-06-04

; EARLIER APPLICATION NUMBER: 60/048,885

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/049,375

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,881

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,880

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,896

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/049,020

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,876

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,895

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,884

Mon Sep 13 07:48:10 2004

us-09-808-388-5.sept04.rni

LOCATION: (1024)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (1032)
OTHER INFORMATION: n equals a,t,g, or c
US-09-205-258-86

Query Match 11.7%; Score 31.8; DB 4; Length 1036;
Best Local Similarity 52.7%; Pred. No. 0.57;
Matches 69; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
QY 128 TCCTGAGTCCACCAACTGACCAACCCATCCCGAGCCTTGTGCTCCTACCTACCCCAACC 187
DB 852 TCCTGAGTCTCCACGCCCTGCGAGCCCTTCTGCTGCTCTCTCCCGGCCCGCAGGC 793
QY 188 TCCAGAGGGAGCAGCTATTTAAGGGAGCAGGAGTGACAGAACACAGACGCGCTGG 247
DB 792 CAGGCGCTGGCGCAGCAATGCAATGGCTGGGGGTGGGATCACCAAGAGAGGCCAAGC 733
QY 248 CATCAACTCT 258
DB 732 CAACCTACCCCT 722

RESULT 8
US-09-328-111-618/c
Sequence 618, Application US/09328111
Patent No. 6262333
GENERAL INFORMATION:
APPLICANT: Endege, Willson O.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Astle, Jon H.
APPLICANT: Burgess, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
APPLICANT: Catino, Theodore J.
APPLICANT: Derti, Adnan
APPLICANT: Ford, Donna M.
APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 618
LENGTH: 305
TYPE: DNA
ORGANISM: Homo sapiens
US-09-328-111-618

Query Match 11.3%; Score 30.6; DB 3; Length 305;
Best Local Similarity 56.4%; Pred. No. 0.83;
Matches 57; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
QY 3 CGGCAAACTGCTGAAATGTTTGGCATCAGCTACTGACACGTAAGTTTCCCAATC 62
DB 217 CGCCAAATAACACGATGTTGTGTAACATCCCCCAGTGGGGCTAGAAATCCCATG 158
QY 63 CTCACTCTGCTGCGCAGCTGATGAGGGAGGAAGGGA 103
DB 157 GTGACCTGTGACCTGCTCCCTGAGACAGGGAGGCCAGGCA 117

RESULT 9
US-09-016-434-1143/c
Sequence 1143, Application US/09016434

Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Selhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1143:
SEQUENCE CHARACTERISTICS:
LENGTH: 2885 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: q1478280
US-09-016-434-1143
Query Match 11.3%; Score 30.6; DB 4; Length 2885;
Best Local Similarity 56.4%; Pred. No. 2.2;
Matches 57; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
QY 3 CGGCAAACTGCTGAAATGTTTGGCATCAGCTACTGACACGTAAGTTTCCCAATC 62
DB 2633 CGCCAAATAACACGATGTTGTGTAACATCCCCCAGTGGGGCTAGAAATCCCATG 2574
QY 63 CTCACTCTGCTGCGCAGCTGATGAGGGAGGAAGGGA 103
DB 2573 GTGACCTGTGACCTGCTCCCTGAGACAGGGAGGCCAGGCA 2533
RESULT 10
US-08-856-444-1
Sequence 1, Application US/08856444
Patent No. 5959081
GENERAL INFORMATION:
APPLICANT: Lecka-Czernik, Beata
TITLE OF INVENTION: No. 5959081el Zinc Binding LIM Protein S2-6
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benjamin Aaron Adler, Ph.D. J.D.
STREET: 8011 Candle Lane
CITY: Houston
STATE: Texas
ZIP: 77071
COMPUTER READABLE FORM:

APPLICANT: Mundy M.D., Gregory R.
APPLICANT: Gosh-Choudhury Ph.D., Nandini
APPLICANT: Feng Ph.D., Jian Q.

	Query Match	10.7%	Score 29;	DB 4;	Length 204;
	Best Local Similarity	57.0%	Pred. No. 2.4;		
	Matches	53;	Conservative	0;	Mismatches 40;
					Indels 0;
					Gaps 0
Qy	4	GGCAAACTCCCTGAAATGTTTGGCATCAGCTACTGACACGTAAGGTTTCCCAATCC	63		
Db	194	GGAACATCTGCCTGCCCAATGGACTGGTGGCTGGCATGGCTTCTAGGATGCTGATGC	135		
Qy	64	TCAACTGTGCTCTGCCAGCTGATCAGGGGAAGG	96		
Db	134	TGCACGGCAGCTTGGAACTGTCAGAGGGGAAGG	102		

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Page 7

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Job time : 43.6131 secs

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OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 09:20:47 ; Search time 50.4382 Seconds
(without alignments)
5187.326 Million cell updates/sec

Title: US-09-808-388-4

Perfect score: 52

Sequence: 1 caaaactagggtcaaaagtca.....caaaactagggtcaaaagtca 52

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 6608766

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
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13: /cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
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16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	52	9	US-09-808-388-4
2	27	51.9	4060	17	US-10-437-963-42345
3	25.2	48.5	42334	12	US-10-052-482-94
4	24.8	47.7	408	15	US-10-214-684A-3
5	24.4	46.9	1350	13	US-10-282-132A-28035
6	23.6	45.4	1821	16	US-10-260-238-1420
7	23.4	45.0	480	13	US-10-027-632-51055
8	23.4	45.0	480	16	US-10-027-632-51055
9	23.4	45.0	517	13	US-10-027-632-51055
10	23.4	45.0	517	16	US-10-027-632-51055
11	23.2	44.6	12596	16	US-10-292-798-889
12	23.2	44.6	12839	15	US-10-017-161-1047
13	23	44.2	559	13	US-10-027-632-245490
14	23	44.2	559	13	US-10-027-632-245491

15	23	44.2	559	16	US-10-027-632-245490
16	23	44.2	559	16	US-10-027-632-245491
17	23	44.2	867	9	US-09-770-443-571
18	23	44.2	3077	15	US-10-128-714-349
19	23	44.2	3078	15	US-10-128-714-5349
20	23	44.2	26047	13	US-10-087-192-598
21	23	44.2	247461	17	US-10-322-281-131
22	22.8	43.8	60	10	US-09-877-705A-142
23	22.8	43.8	60	10	US-09-877-738A-142
24	22.8	43.8	60	13	US-09-947-274-142
25	22.8	43.8	60	17	US-10-779-595-142
26	22.8	43.8	559	13	US-10-027-632-271817
27	22.8	43.8	559	16	US-10-027-632-271817
28	22.8	43.8	632	13	US-10-027-632-271818
29	22.8	43.8	632	16	US-10-027-632-271818
30	22.8	43.8	659	13	US-10-027-632-271818
31	22.8	43.8	659	16	US-10-027-632-11556
32	22.8	43.8	1248	13	US-10-027-632-124870
33	22.8	43.8	1248	16	US-10-027-632-124870
34	22.8	43.8	1418	10	US-09-814-353-21334
35	22.8	43.8	1461	13	US-10-282-122A-22438
36	22.6	43.5	331	17	US-10-437-963-84032
37	22.6	43.5	1035	13	US-10-282-122A-15887
38	22.4	43.1	472	13	US-10-424-599-49385
39	22.4	43.1	971	13	US-10-425-114-11342
40	22.4	43.1	994	13	US-10-424-599-3951
41	22.4	43.1	4290	13	US-10-282-122A-16164
42	22.2	42.7	451	10	US-09-918-995-2661
43	22.2	42.7	456	10	US-09-918-995-15681
44	22.2	42.7	666	13	US-10-027-632-141504
45	22.2	42.7	666	16	US-10-027-632-141504

ALIGNMENTS

RESULT 1
US-09-808-388-4
; Sequence 4, Application US/09808388
; Patent No. US20020081719A1
; GENERAL INFORMATION:
; APPLICANT: Massaad, Charbel
; APPLICANT: Berenbaum, Francis
; APPLICANT: Olivier, Jean-Luc
; APPLICANT: Salvat, Colette
; APPLICANT: Berezat, Gilbert
; TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising them
; TITLE OF INVENTION: their uses
; FILE REFERENCE: ST00010
; CURRENT APPLICATION NUMBER: US/09/808,388
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: FR/00/03262
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/196,959
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 4
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PPPE element
US-09-808-388-4

Query Match 100.0%; Score 52; DB 9; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAAAACTAGGTCAGAGGTCATGCTTTAGGCCCAAACTAGGTCAAAGGTCA 52
DB 1 CAAAACTAGGTCAGAGGTCATGCTTTAGGCCCAAACTAGGTCAAAGGTCA 52

Mon Sep 13 07:48:09 2004

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GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bihain, Bernard
; TITLE OF INVENTION: POLYMORPHIC MARKERS OF THE LSR GENE
; FILE REFERENCE: G-057US04DIV
; CURRENT APPLICATION NUMBER: US/10/214,684A
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US 09/499,522
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 60/119,592
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/144,784
; PRIOR FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent.pm
; SEQ ID NO 3
; LENGTH: 408
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 353
; OTHER INFORMATION: 99-14424-353 : polymorphic base A or G
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: 334_352
; OTHER INFORMATION: 99-14424-353.mis1 real
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: 354_376
; OTHER INFORMATION: 99-14424-353.mis2 potential, complement
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: 1..20
; OTHER INFORMATION: upstream amplification primer
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: 388_408
; OTHER INFORMATION: downstream amplification primer, complement
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 118_118
; OTHER INFORMATION: Any nucleotide.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 155_155
; OTHER INFORMATION: Any nucleotide.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 168_168
; OTHER INFORMATION: Any nucleotide.
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; US-10-214-684A-3
Query Match 47.7%; Score 24.8; DB 15; Length 408;
Best Local Similarity 80.6%; Pred. No. 9.7;
Matches 29; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 12 CAAAGGTCATGCTTTAGGCCCAAACTAGGTCAA 47
Db 348 CACAGCATGGCTTTAGGCCCAAACTAGGTCAA 383

RESULT 5
US-10-282-122A-28035
; Sequence 28035, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari

US-10-437-963-42345/c
; Sequence 42345, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 42345
; LENGTH: 4060
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_45606C.1
;
US-10-437-963-42345
Query Match 51.9%; Score 27; DB 17; Length 4060;
Best Local Similarity 70.6%; Pred. No. 2.5;
Matches 36; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 2 AAAAAGTCAAGTCATGCTTTAGGCCCAAACTAGGTCAAAGGTCA 52
Db 2240 AGAGTGGTCAACAGTCATTTTGTGACGCCCAATGCTAGATAACATGTCA 2190

RESULT 3
US-10-052-482-94
; Sequence 94, Application US/10052482
; Publication No. US20040072264A1
; GENERAL INFORMATION:
; APPLICANT: Engelhard, Eric
; APPLICANT: Morris, David
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71087/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/052,482
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 241
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 94
; LENGTH: 42334
; TYPE: DNA
; ORGANISM: Homo sapiens
;
US-10-052-482-94
Query Match 48.5%; Score 25.2; DB 12; Length 42334;
Best Local Similarity 78.9%; Pred. No. 24;
Matches 30; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CAAAAGTCAAGTCATGCTTTAGGCCCAAACTAGGTCAA 38
Db 2027 CAAAATGGGGTCAAGTTCATGCTTTAGGCCAGATAC 2064

RESULT 4
US-10-214-684A-3
; Sequence 3, Application US/10214684A
; Publication No. US20030190636A1

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; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28035
; LENGTH: 1350
; TYPE: DNA
; ORGANISM: Mycoplasma pneumoniae
; US-10-282-122A-28035

Query Match          46.9%; Score 24.4; DB 13; Length 1350;
Best Local Similarity 69.0%; Pred. No. 19;
Matches 34; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 CAAAGCAGCTCAAGTCTCTTGGCCCAAACTAGGTCAGGTC 50
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 346 CCAAGCAGCTCAAGTCTCTTGGCCCAAACTAGGTCAGGTC 395

RESULT 6
US-10-260-238-1420/c
; Sequence 1420, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
```

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; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 1420
; LENGTH: 1821
; TYPE: DNA
; ORGANISM: Oryza sativa
; US-10-260-238-1420

Query Match          45.4%; Score 23.6; DB 16; Length 1821;
Best Local Similarity 69.6%; Pred. No. 43;
Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 2 AAACTAGGTCAAAGGTCATGCTTTAGGCCCAAACTAGGTCAAA 47
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1645 AAAGCCAAAGTAACAGTTGACATCCATAGGTCACACACTAGGACAAA 1600

RESULT 7
US-10-027-632-51055/c
; Sequence 51055, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51055
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-51055

Query Match          45.0%; Score 23.4; DB 13; Length 480;
Best Local Similarity 81.8%; Pred. No. 36;
Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CAAACTAGGTCAAAGGTCATGCTTTAGGCCCC 33
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 137 CACACCTTGGTCTAAGATAATGCTTTAGGCCCC 105

RESULT 8
US-10-027-632-51055/c
; Sequence 51055, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
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Sequence 82715, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 82715
LENGTH: 517
TYPE: DNA
ORGANISM: Human
US-10-027-632-82715

Query Match 45.0%; Score 23.4; DB 16; Length 517;
Best Local Similarity 81.8%; Pred. No. 37;
Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CAAAACTAGGTCAAAGGTCATGCTTTAGGCC 33
DB 330 CACACCTTGGTCTAAGATAATGCTTTAGGCC 362

RESULT 11
US-10-292-798-889
Sequence 889, Application US/10292798
Publication No. US20030235833A1
GENERAL INFORMATION:
APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: JP 2001-246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 889
LENGTH: 12596
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
LOCATION: source
FEATURE: (1)..(12596)
LOCATION: (1)..(12596)
FEATURE:
NAME/KEY: CDS
LOCATION: (201)..(240)
FEATURE:
NAME/KEY: CDS
LOCATION: (962)..(1276)

PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 51055
LENGTH: 480
TYPE: DNA
ORGANISM: Human
US-10-027-632-51055

Query Match 45.0%; Score 23.4; DB 16; Length 480;
Best Local Similarity 81.8%; Pred. No. 36;
Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CAAAACTAGGTCAAAGGTCATGCTTTAGGCC 33
DB 137 CACACCTTGGTCTAAGATAATGCTTTAGGCC 105

RESULT 9
US-10-027-632-82715
Sequence 82715, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 82715
LENGTH: 517
TYPE: DNA
ORGANISM: Human
US-10-027-632-82715

Query Match 45.0%; Score 23.4; DB 13; Length 517;
Best Local Similarity 81.8%; Pred. No. 37;
Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CAAAACTAGGTCAAAGGTCATGCTTTAGGCC 33
DB 330 CACACCTTGGTCTAAGATAATGCTTTAGGCC 362

RESULT 10
US-10-027-632-82715

Db

348 CACACGACATGGCTTTAGGCCCCCAACAGGTAAAA 383

RESULT 2

PCT-US93-06251-44/c

; Sequence 44, Application PC/TUS9306251

; GENERAL INFORMATION:

; APPLICANT: Wickstrom, Eric and Rife, Jason P.

; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing

; TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates

; NUMBER OF SEQUENCES: 93

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER

; STREET: 400 Garden City Plaza

; CITY: Garden City

; STATE: NY

; COUNTRY: USA

; ZIP: 11530

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/06251

; FILING DATE: 19930630

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Digiglio, Frank S.

; REGISTRATION NUMBER: 31,346

; REFERENCE/DOCKET NUMBER: 8586

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 516-742-4343

; TELEFAX: 516-742-4366

; TELEX: 230 901 SANS UR

; INFORMATION FOR SEQ ID NO: 44:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 232 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

PCT-US93-06251-44

Query Match

Best Local Similarity

Matches

44.6%;

Score 23.2;

DB 5;

Length 232;

31;

Conservative

0;

Mismatches

13;

Indels

0;

Gaps

0;

QY

2 AAAACTAGTCAAGGTCATGCTTTAGGCCCCCAAACTAGGTCA 45

Db

73 AAAAGTAGTCTTTGGTCGGGTTCTTAGGCCAGCACATGGGTCA 30

RESULT 3

US-09-134-000C-1316/c

; Sequence 1316, Application US/09134000C

; Patent No. 6617156

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 032796-032

; CURRENT APPLICATION NUMBER: US/09/134,000C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/055,778

; PRIOR FILING DATE: 1997-08-15

; NUMBER OF SEQ ID NOS: 6812

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 1316

; LENGTH: 900

; TYPE: DNA

; ORGANISM: Enterococcus faecalis

US-09-134-000C-1316

Query Match

Best Local Similarity

Matches

41.9%;

Score 21.8;

DB 3;

Length 72928;

32;

Conservative

0;

Mismatches

17;

Indels

0;

Gaps

0;

QY

2 AAAACTAGTCAAGGTCATGCTTTAGGCCCAAACTAGGTCAAGGT 50

Db

37573 AAAAGTTGATCAATGTCATCTCTTTCTCACGAATCTTGGTCATGTGT 37621

RESULT 5

US-09-023-655-361

; Sequence 361, Application US/09023655

; Patent No. 6607879

; GENERAL INFORMATION:

; APPLICANT: Cocks, Benjamin G.

; APPLICANT: Susan G. Stuart

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

; TITLE OF INVENTION: EXPRESSION

US-09-023-655-361

Query Match

Best Local Similarity

Matches

41.9%;

Score 21.8;

DB 3;

Length 72928;

32;

Conservative

0;

Mismatches

17;

Indels

0;

Gaps

0;

QY

2 AAAACTAGTCAAGGTCATGCTTTAGGCCCAAACTAGGTCAAGGT 50

Db

37573 AAAAGTTGATCAATGTCATCTCTTTCTCACGAATCTTGGTCATGTGT 37621

RESULT 4

US-09-009-913-1

; Sequence 1, Application US/09009913

; Patent No. 6087485

; GENERAL INFORMATION:

; APPLICANT: Axys Pharmaceuticals, Inc.

; TITLE OF INVENTION: Asthma Related Genes

; NUMBER OF SEQUENCES: 339

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Bozicevic & Reed, LLP

; STREET: 285 Hamilton Ave, Suite 200

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/009,913

; FILING DATE: 21-JAN-1998

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Sherwood, Pamela J

; REGISTRATION NUMBER: 36,677

; REFERENCE/DOCKET NUMBER: SEQ-4P

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-327-3231

; TELEFAX: 650-327-3231

; TELEX:

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 72928 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: Genomic DNA

US-09-009-913-1

Query Match

Best Local Similarity

Matches

41.9%;

Score 21.8;

DB 3;

Length 72928;

32;

Conservative

0;

Mismatches

17;

Indels

0;

Gaps

0;

QY

2 AAAACTAGTCAAGGTCATGCTTTAGGCCCAAACTAGGTCAAGGT 50

Db

37573 AAAAGTTGATCAATGTCATCTCTTTCTCACGAATCTTGGTCATGTGT 37621

QY 9 GGTCAAAGGTCATGCTTTAGGCCCAAACTAGG 42

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; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 218
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-328-475C-218

Query Match      40.0%; Score 20.8; DB 4; Length 498;
Best Local Similarity 64.6%; Pred. No. 22;
Matches 31; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY      2 AAACCTAGTCAAAGTCAATGCTCTTTAGGCCCAAACTAGGTCAAAGG 49
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Db      152 AAACCTAGTCAAGTCAATGCTCTTCCACAGTTCCTCAAGCTTAATAAATG 199

RESULT 9
US-09-404-879A-26/c
; Sequence 26, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 541
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-404-879A-26

Query Match      40.0%; Score 20.8; DB 4; Length 541;
Best Local Similarity 78.1%; Pred. No. 22;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      6 CTAGGTCAAAGTCAATGCTCTTTAGGCCCAAAA 37
      |||||
Db      294 CAAGTCAAGGACATGCTTTTAGCCCCCAA 263

RESULT 10
US-09-338-933-26/c
; Sequence 26, Application US/09338933
; Patent No. 6488931
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer Lynn
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
; TITLE OF INVENTION: OVARIAN CANCER
; FILE REFERENCE: 210121.462C1
; CURRENT APPLICATION NUMBER: US/09/338,933
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 541
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-338-933-26

Query Match      40.0%; Score 20.8; DB 4; Length 541;
Best Local Similarity 78.1%; Pred. No. 22;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      6 CTAGGTCAAAGTCAATGCTCTTTAGGCCCAAAA 37
      |||||
Db      294 CAAGTCAAGGACATGCTTTTAGCCCCCAA 263

RESULT 11
US-09-215-681-26/c
; Sequence 26, Application US/09215681A
; Patent No. 6528253
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Frudakis, Tony N.
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: OF OVARIAN CANCER
; FILE REFERENCE: 210121.463
; CURRENT APPLICATION NUMBER: US/09/215,681A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 310
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 541
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-215-681-26

Query Match      40.0%; Score 20.8; DB 4; Length 541;
Best Local Similarity 78.1%; Pred. No. 22;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      6 CTAGGTCAAAGTCAATGCTCTTTAGGCCCAAAA 37
      |||||
Db      294 CAAGTCAAGGACATGCTTTTAGCCCCCAA 263

RESULT 12
US-09-216-003A-26/c
; Sequence 26, Application US/09216003A
; Patent No. 6670463
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Frudakis, Tony N.
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF OVARIAN CANCER
; FILE REFERENCE: 210121.462
; CURRENT APPLICATION NUMBER: US/09/216,003A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 310
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 541
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-216-003A-26

Query Match      40.0%; Score 20.8; DB 4; Length 541;
Best Local Similarity 78.1%; Pred. No. 22;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      6 CTAGGTCAAAGTCAATGCTCTTTAGGCCCAAAA 37
      |||||
Db      294 CAAGTCAAGGACATGCTTTTAGCCCCCAA 263

RESULT 13
US-09-328-475C-335/c
; Sequence 335, Application US/09328475C
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 09:20:47 ; Search time 39.7686 Seconds
(without alignments)
5187.326 Million cell updates/sec

Title: US-09-808-388-3
Perfect score: 41
Sequence: 1 caaaactagggtcaaaagggtca.....caaaactagggtcaaaagggtca 41

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 6608766

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
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- 13: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	41	100.0	332	9	US-09-808-388-6
3	29	70.7	60	10	US-09-877-705A-142
4	29	70.7	60	10	US-09-877-738A-142
5	29	70.7	60	13	US-09-947-274-142
6	29	70.7	60	17	US-10-779-595-142
7	25	61.0	38	9	US-09-808-388-2
8	24.6	60.0	85859	13	US-10-087-192-562
9	23.6	57.6	177556	10	US-09-952-213D-6
10	23.2	56.6	582	13	US-10-424-599-53103
11	23	56.1	580073	15	US-10-205-220-1
12	22.4	54.6	862	13	US-10-424-599-139279
13	22.4	54.6	3295	10	US-09-952-267-8
14	22.4	54.6	3349	10	US-09-952-267-2

15	22.2	54.1	3130	13	US-10-424-599-56034	Sequence 56034, A
C 16	22	53.7	2940917	13	US-10-027-632-174763	Sequence 174763, A
C 17	22	53.7	2940917	16	US-10-027-632-174763	Sequence 174763, A
C 18	21.6	52.7	785	13	US-10-027-632-158188	Sequence 158188, A
C 19	21.6	52.7	785	13	US-10-027-632-158188	Sequence 158188, A
C 20	21.6	52.7	785	16	US-10-027-632-158189	Sequence 158189, A
C 21	21.6	52.7	785	16	US-10-027-632-158189	Sequence 158189, A
C 22	21.6	52.7	715517	13	US-10-027-632-53712	Sequence 53712, A
C 23	21.6	52.7	715517	16	US-10-027-632-53712	Sequence 53712, A
C 24	21.4	52.2	430	15	US-10-102-524-1082	Sequence 1082, A
C 25	21.4	52.2	474	10	US-09-918-995-29668	Sequence 29668, A
C 26	21.4	52.2	512	15	US-10-102-524-433	Sequence 433, App
C 27	21.4	52.2	634	15	US-10-060-036-215	Sequence 215, App
C 28	21.4	52.2	851	17	US-10-437-963-50885	Sequence 50885, A
C 29	21.4	52.2	910	15	US-10-190-312A-86	Sequence 86, Appl
C 30	21.4	52.2	978	13	US-10-027-632-324444	Sequence 324444, A
C 31	21.4	52.2	978	16	US-10-027-632-324444	Sequence 324444, A
C 32	21.4	52.2	2595	15	US-10-106-698-451	Sequence 451, App
C 33	21.4	52.2	2930	9	US-09-960-253-156	Sequence 156, App
C 34	21.4	52.2	2930	17	US-10-450-826-88	Sequence 88, Appl
C 35	21.4	52.2	3044	9	US-09-880-107-3718	Sequence 3718, App
C 36	21.4	52.2	3044	17	US-10-450-826-87	Sequence 87, Appl
C 37	21.4	52.2	3044	17	US-10-450-826-87	Sequence 84, Appl
C 38	21.4	52.2	3047	9	US-09-864-864-329	Sequence 329, App
C 39	21.4	52.2	3064	15	US-10-007-926A-53	Sequence 53, Appl
C 40	21.4	52.2	3072	17	US-10-450-826-89	Sequence 89, Appl
C 41	21.4	52.2	3115	9	US-09-925-299-123	Sequence 123, App
C 42	21.4	52.2	3115	10	US-09-925-299-123	Sequence 123, App
C 43	21.4	52.2	3166	16	US-10-159-563-357	Sequence 357, App
C 44	21.4	52.2	5253	13	US-10-424-599-131924	Sequence 131924, A
C 45	21.4	52.2	26345	13	US-10-087-192-1705	Sequence 1705, Ap

ALIGNMENTS

RESULT 1
US-09-808-388-3
; Sequence 3, Application US/09808388
; Patent No. US20020081719A1

; GENERAL INFORMATION:
; APPLICANT: Massaad, Charbel
; APPLICANT: Berenbaum, Francis
; APPLICANT: Olivier, Jean-Luc
; APPLICANT: Salvat, Colette
; APPLICANT: Berezat, Gilbert
; TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising them
; TITLE OF INVENTION: their uses
; FILE REFERENCE: ST00010
; CURRENT APPLICATION NUMBER: US/09/808,388
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: FR/00/03262
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/196,959
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 3

; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PPSE element
US-09-808-388-3

Query Match 100.0%; Score 41; DB 9; Length 41;
Best Local Similarity 100.0%; Pred. No. 5.3e-06;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAACTAGGTCAAAAGGTCAATCAAACTAGGTCAAAAGGTCA 41
DB 1 CAAAACTAGGTCAAAAGGTCAATCAAACTAGGTCAAAAGGTCA 41

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;
; APPLICANT: Li, Xianqiang
;
; TITLE OF INVENTION: METHOD, ARRAY AND KIT FOR DETECTING ACTIVATED TRANSCRIPTION FACTOR
;
; FILE REFERENCE: 26757-702.301
;
; CURRENT APPLICATION NUMBER: US/10/779,595
;
; CURRENT FILING DATE: 2004-02-13
;

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; PRIOR APPLICATION NUMBER: 09/877,243
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 142
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hybridization probe MP68
US-10-779-595-142

Query Match 70.7%; Score 29; DB 17; Length 60;
Best Local Similarity 97.6%; Pred. No. 0.19;
Matches 40; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CAAACTAGTCAAGGTCATCAAACTAGGTCAAAAGGTCA 41
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Db 60 CAAACTAGTCAAGGTCATCAAACTAGGTCAAAAGGTCA 21
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RESULT 7

US-09-808-388-2
; Sequence 2, Application US/09808388
; Patent No. US20020081719A1
; GENERAL INFORMATION:
; APPLICANT: Massaad, Charbel
; APPLICANT: Berenbaum, Francis
; APPLICANT: Olivier, Jean-Luc
; APPLICANT: Salvat, Colette
; APPLICANT: Berezat, Gilbert
; TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising them
; FILE REFERENCE: ST00010
; CURRENT APPLICATION NUMBER: US/09/808,388
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: FR/00/03262
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/196,959
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PPRE element
US-09-808-388-2

Query Match 61.0%; Score 25; DB 9; Length 38;
Best Local Similarity 92.7%; Pred. No. 5.5;
Matches 38; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 CAAACTAGTCAAGGTCATCAAACTAGGTCAAAAGGTCA 41
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Db 1 CAAACTAGTCAAGG---TCAAACTAGGTCAAAAGGTCA 38
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RESULT 8

US-10-087-192-562/c
; Sequence 562, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 562
; LENGTH: 85859
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)---(85859)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-562

Query Match 60.0%; Score 24.6; DB 13; Length 85859;
Best Local Similarity 76.9%; Pred. No. 56;
Matches 30; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 3 AAACCTAGGTCAAGGTCATCAAACTAGGTCAAAAGGTCA 41
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Db 9276 AAACATCTCAAGGACATAAACACTATGTCAAGGACA 9238
|||||

RESULT 9

US-09-952-213D-6/c
; Sequence 6, Application US/09952213D
; Publication No. US20030096240A1
; GENERAL INFORMATION:
; APPLICANT: MURAD, FERID
; APPLICANT: SHARINA, IRAIDA G.
; APPLICANT: KRUMENACKER, J. S.
; APPLICANT: MARTIN, E.
; TITLE OF INVENTION: GENOMIC ORGANIZATION OF MOUSE AND HUMAN SCG
; FILE REFERENCE: UTSH:252US
; CURRENT APPLICATION NUMBER: US/09/952,213D
; CURRENT FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 177556
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (2293..144567)
; OTHER INFORMATION: N = A, C, T/U OR G
US-09-952-213D-6

Query Match 57.6%; Score 23.6; DB 10; Length 177556;
Best Local Similarity 76.3%; Pred. No. 1.6e+02;
Matches 29; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 AAACCTAGGTCAAGGTCATCAAACTAGGTCAAAAGGT 39
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Db 120237 AAATCCAGGTGAGGTCATGAAGGTTGGGCAAGGT 120200
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RESULT 10

US-10-424-599-53103/c
; Sequence 53103, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 53103

Query Match 54.6%; Score 22.4; DB 13; Length 862;
Best Local Similarity 72.5%; Pred. No. 1.2e+02;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 2 AAAAAGTGGTCAAAAGGTCATCAAAAGTGGTCAAAAGGTC 41
DB 631 AAGATGATGACAAAGGTCATGACAAAAGGTC 592
RESULT 13
US-09-952-267-8
; Sequence 8, Application US/09952267
; Publication No. US20030032772A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, ERIC J.
; APPLICANT: AEBI, CHRISTOPH
; APPLICANT: COPE, LESLIE D.
; APPLICANT: MACIVER, ISOBEL
; APPLICANT: FISKE, MICHAEL J.
; APPLICANT: FREDENBURG, ROSS A.
; TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
; FILE REFERENCE: AMCY:024
; CURRENT APPLICATION NUMBER: US/09/952,267
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 09/336,447
; PRIOR FILING DATE: 1999-06-21
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 3295
; TYPE: DNA
; ORGANISM: Moraxella catarrhalis
US-09-952-267-8
Query Match 54.6%; Score 22.4; DB 10; Length 3295;
Best Local Similarity 72.5%; Pred. No. 1.6e+02;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 1 CAAAAGTGGTCAAAAGGTCATCAAAAGTGGTCAAAAGGTC 40
DB 2118 CAAGATATATCAAGATCTTCAGAGGAGGTCAGAGGTC 2157
RESULT 14
US-09-952-267-2
; Sequence 2, Application US/09952267
; Publication No. US20030032772A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, ERIC J.
; APPLICANT: AEBI, CHRISTOPH
; APPLICANT: COPE, LESLIE D.
; APPLICANT: MACIVER, ISOBEL
; APPLICANT: FISKE, MICHAEL J.
; APPLICANT: FREDENBURG, ROSS A.
; TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
; FILE REFERENCE: AMCY:024
; CURRENT APPLICATION NUMBER: US/09/952,267
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 09/336,447
; PRIOR FILING DATE: 1999-06-21
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 3349
; TYPE: DNA
; ORGANISM: Moraxella catarrhalis
US-09-952-267-2
Query Match 54.6%; Score 22.4; DB 10; Length 3349;
Best Local Similarity 72.5%; Pred. No. 1.7e+02;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 1 CAAAAGTGGTCAAAAGGTCATCAAAAGTGGTCAAAAGGTC 40

Query Match 56.6%; Score 23.2; DB 13; Length 582;
Best Local Similarity 77.8%; Pred. No. 53;
Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 CAAAAGTGGTCAAAAGGTCATCAAAAGTGGTCAAA 36
DB 527 CAACCTAGCTCAAAAGGTAACCATTAAGTGGTATA 492
RESULT 11
US-10-205-220-1/c
; Sequence 1, Application US/10205220
; Publication No. US20030170663A1
; GENERAL INFORMATION:
; APPLICANT: Fraser et al.
; TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome, Fragment
; FILE REFERENCE: PB193PID1
; CURRENT APPLICATION NUMBER: US/10/205,220
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 06/545,528
; PRIOR FILING DATE: 1995-10-19
; PRIOR APPLICATION NUMBER: US 08/488,018
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/473,545
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 580073
; TYPE: DNA
; ORGANISM: Mycoplasma genitalium
US-10-205-220-1
Query Match 56.1%; Score 23; DB 15; Length 580073;
Best Local Similarity 74.4%; Pred. No. 3.6e+02;
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 3 AAAGTGGTCAAAAGGTCATCAAAAGTGGTCAAAAGGTC 41
DB 21505 AAATTTGGTAAACAAATCAAAACAGATCAAGATCA 21467
RESULT 12
US-10-424-599-139279/c
; Sequence 139279, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 139279
; LENGTH: 862
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_96777C.1
US-10-424-599-139279

Db 1311 CAAGATGATCAAGATCTTCAGAGGAGGTGAAGGTC 1350

RESULT 15

US-10-424-599-56034
; Sequence 56034, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF FILING DATE: 2003-04-28
; SEQ ID NO 56034
; LENGTH: 3130
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(3130)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_2160C.1
US-10-424-599-56034

Query Match 54.1%; Score 22.2; DB 13; Length 3130;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 13 AAGGTCATCAAACTAGGTCAAGGT 39
Db 1451 AAGGTCATCAAACTGGTCAAGTT 1477

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Job time : 45.7686 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 08:16:17 ; Search time 6.447 Seconds
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3529.238 Million cell updates/sec

Title: US-09-808-388-3
Perfect score: 41
Sequence: 1 caaaactaggtcaaaagggtca.....caaaactaggtcaaaagggtca 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/2/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PTCUS_COMB.seq: *
6: /cgn2_6/ptodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	23	56.1	580073	4	US-08-545-528D-1
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3	22.4	54.6	3349	4	US-09-336-447A-2
C 4	21.2	51.7	1305	4	US-09-328-352-3178
C 5	21	51.2	865	3	US-09-328-111-128
6	20.4	49.8	910	3	US-09-328-111-129
C 7	20.4	49.8	3900	1	US-08-123-343A-6
C 8	20.2	49.3	1140	4	US-09-328-352-1678
9	20.2	49.3	2308	1	US-07-686-591-3
10	20.2	49.3	2308	1	US-07-970-715-3
C 11	20	48.8	966	4	US-09-328-352-1604
12	20	48.8	1200	4	US-09-222-938A-47
C 13	19.8	48.3	1797	2	US-08-366-490-5
14	19.8	48.3	1797	3	US-08-860-483A-5
15	19.8	48.3	1900	2	US-08-366-490-7
16	19.8	48.3	1900	3	US-08-860-483A-8
17	19.8	48.3	1900	3	US-08-860-483A-9
C 18	19.8	48.3	3172	4	US-09-976-594-400
C 19	19.8	48.3	15894	1	US-08-348-891A-1
C 20	19.8	48.3	15894	1	US-08-905-817-1
21	19.8	48.3	19056	3	US-09-272-032-8
22	19.8	48.3	19056	4	US-09-443-218-8
C 23	19.6	47.8	2868	2	US-08-389-564B-3
C 24	19.6	47.8	2868	3	US-08-466-047B-3
25	19.4	47.3	384	4	US-09-107-532A-1817
C 26	19.4	47.3	1143	4	US-09-170-496D-61
C 27	19.4	47.3	1143	4	US-09-170-496D-197

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c 28 19.4 47.3 1317 4 US-09-328-352-2385 Sequence 2385, Ap
c 29 19.4 47.3 1464 4 US-09-149-045-1 Sequence 1, Appli
c 30 19.4 47.3 1583 4 US-09-016-434-1365 Sequence 1365, Ap
c 31 19.4 47.3 1749 4 US-09-081-149-6 Sequence 6, Appli
c 32 19.4 47.3 1758 4 US-09-255-518C-4 Sequence 4, Appli
c 33 19.4 47.3 1834 4 US-08-843-472-5 Sequence 5, Appli
c 34 19.4 47.3 1872 1 US-08-153-848-39 Sequence 39, Appli
c 35 19.4 47.3 1872 3 US-09-299-843A-39 Sequence 39, Appli
c 36 19.4 47.3 1872 4 US-09-088-337B-39 Sequence 70, Appli
c 37 19.4 47.3 1872 5 PCT-US93-11153-39 Sequence 21, Appli
c 38 19.4 47.3 2462 4 US-09-220-132-79 Sequence 97, Appli
c 39 19.4 47.3 10432 4 US-09-919-172-97 Sequence 97, Appli
c 40 19.4 47.3 10432 4 US-09-976-594-21 Sequence 21, Appli
c 41 19.2 46.8 132 1 US-08-053-171-23 Sequence 23, Appli
c 42 19.2 46.8 849 4 US-09-540-236-656 Sequence 656, App
c 43 19.2 46.8 1001 4 US-09-641-638-480 Sequence 480, App
c 44 19.2 46.8 1001 4 US-09-641-638-481 Sequence 481, App
c 45 19.2 46.8 1001 4 US-09-641-638-482 Sequence 482, App

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ALIGNMENTS

RESULT 1

US-08-545-528D-1/c
; Sequence 1, Application US/08545528D
; Patent No. 6537773

; GENERAL INFORMATION:

; APPLICANT: Fraser et al.

; TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome, Fragment

; Patent No. 6537773

; FILE REFERENCE: PB193P1

; CURRENT APPLICATION NUMBER: US/08/545,528D

; CURRENT FILING DATE: 1995-10-19

; PRIOR APPLICATION NUMBER: US 08/488,018

; PRIOR FILING DATE: 1995-06-07

; PRIOR APPLICATION NUMBER: US 08/473,545

; PRIOR FILING DATE: 1995-06-07

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 580073

; TYPE: DNA

; ORGANISM: Mycoplasma genitalium

US-08-545-528D-1

Query Match 56.1%; Score 23; DB 4; Length 580073;
Best Local Similarity 74.4%; Pred. No. 14;
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 3 AAACAGGTCAAGGTCAATCAAAAGTGGTCAAGGTCA 41

Db 21505 AAATTGGTAAACAAATCAAAACAGATCAAGATCA 21467

RESULT 2

US-09-336-447A-8

; Sequence 8, Application US/09336447A

; Patent No. 6310190

; GENERAL INFORMATION:

; APPLICANT: HANSEN, ERIC J.

; APPLICANT: ABEI, CHRISTOPH

; APPLICANT: COPE, LESLIE D.

; APPLICANT: MACIVER, ISOBEL

; APPLICANT: FISKE, MICHAEL J.

; APPLICANT: FREDENBURG, ROSS A.

; TITLE OF INVENTION: USP2 ANTIGENS OF MORAXELLA CATARRHALIS

; FILE REFERENCE: AMCY:024

; CURRENT APPLICATION NUMBER: US/09/336,447A

; CURRENT FILING DATE: 1999-06-21

; NUMBER OF SEQ ID NOS: 98

; SOFTWARE: PatentIn Ver. 2.1

RESULT 11
US-09-328-352-1604
; Sequence 1604, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 1604
; LENGTH: 966
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-1604
Query Match 48.8%; Score 20; DB 4; Length 966;
Best Local Similarity 72.2%; Pred. No. 42;
Matches 26; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1 CAAAACTAGGTCAAAGGTCATCAAACTAGGTCATAA 36
Db 161 CAAAGCTATTATAAAGGCTTCATAAAATTGATGAAA 196
RESULT 12
US-09-222-938A-47/c
; Sequence 47, Application US/09222938A
; Patent No. 6437108
; GENERAL INFORMATION:
; APPLICANT: Youngman, Philip
; APPLICANT: Fritz, Christian
; APPLICANT: Murphy, Christopher
; APPLICANT: Guzman, Luz-Maria
; TITLE OF INVENTION: ESSENTIAL BACTERIAL GENES AND THEIR USE
; FILE REFERENCE: 07334/060001
; CURRENT APPLICATION NUMBER: US/09/222,938A
; CURRENT FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 47
; LENGTH: 1200
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (95)...(1126)
US-09-222-938A-47
Query Match 48.8%; Score 20; DB 4; Length 1200;
Best Local Similarity 72.2%; Pred. No. 45;
Matches 26; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 6 CTAGGTCAAAGGTCATCAAACTAGGTCATAAAGGTCA 41
Db 542 CTGGTCATAAATCCTTCAGATTGTTCAAGGTTA 507
RESULT 13
US-08-366-490-5
; Sequence 5, Application US/08366490
; Patent No. 5877403
; GENERAL INFORMATION:
; APPLICANT: McMaster, J. Russell
; APPLICANT: Boeshore, Maury L
; APPLICANT: Tricoli, David M
; APPLICANT: Reynolds, John F
; APPLICANT: Carney, Kim J
; TITLE OF INVENTION: PAPAYA RINGSPOT VIRUS PROTEASE GENE
; NUMBER OF SEQUENCES: 10

US-07-686-591-3
Query Match 49.3%; Score 20.2; DB 1; Length 2308;
Best Local Similarity 68.3%; Pred. No. 44;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 1 CAAAACTAGGTCAAAGGTCATCAAACTAGGTCATAAAGGTCA 41
Db 1539 CAAAGAGGAGACCAAGGCTTCATAAACCCGTGTCATGATCA 1579
RESULT 10
US-07-970-715-3
; Sequence 3, Application US/07970715
; Patent No. 5245011
; GENERAL INFORMATION:
; APPLICANT: Tiberi, Mario
; APPLICANT: Jarvie, Keith R.
; APPLICANT: Caron, Marc G.
; TITLE OF INVENTION: Cloned Gene Encoding Rat D1B Dopamine Receptor
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park and Gibson
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5245011th Carolina
; COUNTRY: U.S.A.
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/970,715
; FILING DATE: 19921103
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/686,591
; FILING DATE: 4/6/91
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5405.24
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2308 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 694..2118
; OTHER INFORMATION:
US-07-970-715-3
Query Match 49.3%; Score 20.2; DB 1; Length 2308;
Best Local Similarity 68.3%; Pred. No. 44;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 1 CAAAACTAGGTCAAAGGTCATCAAACTAGGTCATAAAGGTCA 41
Db 1539 CAAAGAGGAGACCAAGGCTTCATAAACCCGTGTCATGATCA 1579

/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
/ STREET: 277 Park Avenue
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10172-0194
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ FILING DATE: 30-DEC-1994
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fitzpatrick, Cella, Harper, and Scinto
/ REFERENCE/DOCKET NUMBER: 4869
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 212-758-2400
/ TELEFAX: 212-758-2982
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1797 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: internal
/ ORIGINAL SOURCE:
/ ORGANISM: PAPAYA RINGSPOT VIRUS
/ STRAIN: P-TYPE
/ INDIVIDUAL ISOLATE: USA (HA attenuated)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 3..1782
/ FEATURE:
/ NAME/KEY: mat_peptide
/ LOCATION: 3..191
/ FEATURE:
/ NAME/KEY: mat_peptide
/ LOCATION: 192..362
/ FEATURE:
/ NAME/KEY: mat_peptide
/ LOCATION: 363..1643
/ FEATURE:
/ NAME/KEY: mat_peptide
/ LOCATION: 1644..1782
/ US-08-366-490-5

Query Match 48.3%; Score 19.8; DB 2; Length 1797;
Best Local Similarity 69.2%; Pred.No. 60;
Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 1 CAAAGCTAGGTCAGGTCATCAAACTAGGTCAAAGGT 39
Db 1214 CAGAGCTAGGTTTGGGCCATGAAGCTGGGACAAAGGT 1252

RESULT 14
US-08-860-483A-5
; Sequence 5, Application US/08860483A
; Patent No. 6048384
; GENERAL INFORMATION:
; APPLICANT: McMaster, J. R.
; APPLICANT: Boeshore, Maury L.
; APPLICANT: Tricoli, David M.
; APPLICANT: Reynolds, John F.
; APPLICANT: Carney, Kim J.
; APPLICANT: Slighton, Jerry L.

/ APPLICANT: Gonsalves, Dennis
/ TITLE OF INVENTION: Papaya Ringspot Virus N1a Protease Gene
/ NUMBER OF SEQUENCES: 13
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Rocky, Milnanow & Katz
/ STREET: 180 N. Stetson Avenue, 2 Prudential Plaza,
/ CITY: Chicago
/ STATE: IL
/ COUNTRY: USA
/ ZIP: 60601
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ FILING DATE: 26-JUN-1997
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mueller, Lisa V.
/ REGISTRATION NUMBER: 38,978
/ REFERENCE/DOCKET NUMBER: SVS3801P0091US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 3126165400
/ TELEFAX: 3126165460
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1797 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: not relevant
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 3..1779
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1782..1797
/ US-08-860-483A-5

Query Match 48.3%; Score 19.8; DB 3; Length 1797;
Best Local Similarity 69.2%; Pred.No. 60;
Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 1 CAAAGCTAGGTCAGGTCATCAAACTAGGTCAAAGGT 39
Db 1214 CAGAGCTAGGTTTGGGCCATGAAGCTGGGACAAAGGT 1252

RESULT 15
US-08-366-490-7
; Sequence 7, Application US/08366490
; Patent No. 5877403
; GENERAL INFORMATION:
; APPLICANT: McMaster, J. Russell
; APPLICANT: Boeshore, Maury L.
; APPLICANT: Tricoli, David M.
; APPLICANT: Reynolds, John F.
; APPLICANT: Carney, Kim J.
/ TITLE OF INVENTION: PAPAYA RINGSPOT VIRUS PROTEASE GENE
/ NUMBER OF SEQUENCES: 10
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
/ STREET: 277 Park Avenue
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10172-0194
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible

Mon Sep 13 07:48:09 2004

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/366,490
FILING DATE: 30-DEC-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Fitzpatrick, Cella, Harper, and Scinto
REFERENCE/DOCKET NUMBER: 4869
TELEPHONE: 212-758-2400
TELEFAX: 212-758-2982
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1900 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: PAPAYA RINGSPOT VIRUS
STRAIN: P-TYPE
INDIVIDUAL ISOLATE: Hawaii
FEATURE:
NAME/KEY: CDS
LOCATION: 3..1900
PUBLICATION INFORMATION:
AUTHORS: Yeh, SD
AUTHORS: Jan, F
AUTHORS: Chiang, C
AUTHORS: Doong, T
AUTHORS: Chen, M
AUTHORS: Chung, P
AUTHORS: Bau, H
TITLE: Complete nucleotide sequence and genetic
TITLE: organization of papaya ringspot virus.
JOURNAL: J. Gen. Virol.
VOLUME: 73
PAGES: 2531-
DATE: 1992
US-08-366-490-7

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Query Match      48.3%; Score 19.8; DB 2; Length 1900;
Best Local Similarity 69.2%; Pred. No. 60;
Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Qy      1 CAAAACCTAGGTCAAAGTCTATCAAACTAGGTCAAAGGT 39
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Db     1226 CAGAGCTAGGTTTAGGGCCATGAAGCTGGGGACAGGT 1264

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Search completed: September 11, 2004, 09:33:13
Job time : 8.447 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 09:20:47 ; Search time 36.8587 Seconds
(without alignments)
5187.326 Million cell updates/sec

Title: US-09-808-388-2

Perfect score: 38

Sequence: 1 caaaactaggctcaaaaggctcaaaactaggctcaaaagtca 38

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 6608766

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	38	9	US-09-808-388-2
2	26	68.4	60	10	US-09-877-705A-142
3	26	68.4	60	10	US-09-877-738A-142
4	26	68.4	60	13	US-09-947-274-142
5	26	68.4	60	17	US-10-779-595-142
6	25	65.8	41	9	US-09-808-388-3
7	25	65.8	332	9	US-09-808-388-6
8	23.6	62.1	2113	15	US-10-153-668-319
9	23.6	62.1	2886	16	US-10-264-049-778
10	23.6	62.1	2926	16	US-10-094-749-46
11	22.6	59.5	634	17	US-10-389-566-61
12	21.6	56.8	467	13	US-10-027-632-17516
13	21.6	56.8	467	16	US-10-027-632-17516
14	21.6	56.8	1161	17	US-10-437-963-27118

15	21.6	56.8	2506	13	US-10-302-172-879	Sequence 879, App
16	21.6	56.8	3051	15	US-10-198-846-11260	Sequence 11260, A
17	21.6	56.8	73634	12	US-10-052-482-121	Sequence 121, App
18	21.6	56.8	397658	9	US-09-813-320-3	Sequence 3, Appl1
19	21.4	56.3	14554	9	US-09-764-860-1054	Sequence 1054, Ap
20	21.4	56.3	14554	15	US-10-074-095-1054	Sequence 1054, Ap
21	21.4	56.3	14554	16	US-10-212-872-1054	Sequence 10, Appl
22	21.4	56.3	29105	15	US-10-004-113-10	Sequence 96690, A
23	21.2	55.8	344	13	US-10-424-599-96690	Sequence 8109, Ap
24	21	55.3	511	17	US-10-021-323-8109	Sequence 13618, A
25	21	55.3	583	13	US-10-027-632-13618	Sequence 243, App
26	21	55.3	583	16	US-10-027-632-13618	Sequence 13660, A
27	21	55.3	75899	9	US-09-854-883-243	Sequence 13660, A
28	21	55.3	75899	16	US-10-360-510-243	Sequence 162, App
29	20.8	54.7	456	13	US-10-027-632-13660	Sequence 241240, A
30	20.8	54.7	456	16	US-10-027-632-13660	Sequence 10313, A
31	20.8	54.7	512	13	US-09-854-867-162	Sequence 10313, A
32	20.8	54.7	598	13	US-10-027-632-241240	Sequence 10314, A
33	20.8	54.7	598	16	US-10-027-632-241240	Sequence 10314, A
34	20.8	54.7	1089	13	US-10-027-632-10313	Sequence 10314, A
35	20.8	54.7	1089	13	US-10-027-632-10313	Sequence 10314, A
36	20.8	54.7	1089	16	US-10-027-632-10313	Sequence 10314, A
37	20.8	54.7	1089	16	US-10-027-632-10313	Sequence 10314, A
38	20.8	54.7	188794	17	US-10-322-696-112	Sequence 112, App
39	20.6	54.2	404	12	US-09-732-627A-2042	Sequence 2042, Ap
40	20.6	54.2	426	15	US-10-362-939-7	Sequence 15965, A
41	20.6	54.2	503	17	US-10-021-323-15965	Sequence 14360, A
42	20.6	54.2	529	17	US-10-021-323-14360	Sequence 211395, A
43	20.6	54.2	585	13	US-10-027-632-211395	Sequence 211395, A
44	20.6	54.2	585	16	US-10-027-632-211395	Sequence 99872, A
45	20.6	54.2	656	13	US-10-027-632-99872	

ALIGNMENTS

RESULT 1
US-09-808-388-2
; Sequence 2, Application US/09808388
; Patent No. US20020081719A1
; GENERAL INFORMATION:
; APPLICANT: Massaad, Charbel
; APPLICANT: Berenbaum, Francis
; APPLICANT: Olivier, Jean-Luc
; APPLICANT: Salvat, Colette
; APPLICANT: Berezziat, Gilbert
; TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising them
; TITLE OF INVENTION: their uses
; FILE REFERENCE: ST00010
; CURRENT APPLICATION NUMBER: US/09/808,388
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: FR/00/03262
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/196,959
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PPRE element
US-09-808-388-2

Query Match 100.0%; Score 38; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 8.1e-05;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAACCTAGGTCAAAAGTCAAAAGTCAAAAGTCA 38

Db 1 CAAAACCTAGGTCAAAAGTCAAAAGTCAAAAGTCA 38

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; PRIOR APPLICATION NUMBER: US 09/877,243
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/877,403
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/877,705
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 142
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hybridization probe MP68
US-09-947-274-142

Query Match      68.4%; Score 26; DB 13; Length 60;
Best Local Similarity 95.0%; Pred. No. 2.6;
Matches 38; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY      1 CAAAACCTAGGTCAAAGGT--CAAAACCTAGGTCAAAGGTCA 38
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Db      60 CAAAACCTAGGTCAAAGGTCAAAAACCTAGGTCAAAGGTCA 21

RESULT 5
US-10-779-595-142/c
; Sequence 142, Application US/10779595
; Publication No. US20040132090A1
; GENERAL INFORMATION:
; APPLICANT: Li, Xianqiang
; TITLE OF INVENTION: METHOD, ARRAY AND KIT FOR DETECTING ACTIVATED TRANSCRIPT
; FILE REFERENCE: 26757-702.301
; CURRENT APPLICATION NUMBER: US/10/779,595
; CURRENT FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: 09/877,243
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 142
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hybridization probe MP68
US-10-779-595-142

Query Match      68.4%; Score 26; DB 17; Length 60;
Best Local Similarity 95.0%; Pred. No. 2.6;
Matches 38; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY      1 CAAAACCTAGGTCAAAGGT--CAAAACCTAGGTCAAAGGTCA 38
      |||||||
Db      60 CAAAACCTAGGTCAAAGGTCAAAAACCTAGGTCAAAGGTCA 21

RESULT 6
US-09-808-388-3
; Sequence 3, Application US/09808388
; Patent No. US20020081719A1
; GENERAL INFORMATION:
; APPLICANT: Massaad, Charbel
; APPLICANT: Berenbaum, Francis
; APPLICANT: Olivier, Jean-Luc
; APPLICANT: Salvat, Colette
; APPLICANT: Berezziat, Gilbert
; TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising
; TITLE OF INVENTION: their uses
; FILE REFERENCE: ST00010
; CURRENT APPLICATION NUMBER: US/09/808,388
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: FR/00/03262
; PRIOR FILING DATE: 2000-03-14

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; PRIOR APPLICATION NUMBER: US 60/196,959
 ; PRIOR FILING DATE: 2000-04-13
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 41
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: PPRE element
 US-09-808-388-3

Query Match 65.8%; Score 25; DB 9; Length 41;
 Best Local Similarity 92.7%; Pred. No. 5.7;
 Matches 38; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 CAAAACTAGGTCAAAGG---TCAAACTAGGTCAAAGGTCA 38
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 Db 1 CAAAACTAGGTCAAAGGTCAATCAAACTAGGTCAAAGGTCA 41
 |||||

RESULT 7

US-09-808-388-6

; Sequence 6, Application US/09808388
 ; Patent No. US20020081719A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Massaad, Charbel
 ; APPLICANT: Berenbaum, Francis
 ; APPLICANT: Olivier, Jean-Luc
 ; APPLICANT: Salvat, Colette
 ; APPLICANT: Bereziat, Gilbert
 ; TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising them
 ; FILE OF INVENTION: their uses
 ; FILE REFERENCE: ST00010
 ; CURRENT APPLICATION NUMBER: US/09/808,388
 ; CURRENT FILING DATE: 2001-09-20
 ; PRIOR APPLICATION NUMBER: FR/00/03262
 ; PRIOR FILING DATE: 2000-03-14
 ; PRIOR FILING DATE: 2000-04-13
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 6
 ; LENGTH: 332
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: PPRE/PLA2s hybrid promoter
 US-09-808-388-6

Query Match 65.8%; Score 25; DB 9; Length 332;
 Best Local Similarity 92.7%; Pred. No. 8.6;
 Matches 38; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 CAAAACTAGGTCAAAGG---TCAAACTAGGTCAAAGGTCA 38
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 Db 13 CAAAACTAGGTCAAAGGTCAATCAAACTAGGTCAAAGGTCA 53
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RESULT 8

US-10-153-668-319/c

; Sequence 319, Application US/10153668
 ; Publication No. US20030092616A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HONDA, Goichi
 ; APPLICANT: MATSUDA, Akio
 ; APPLICANT: MURAMATSU, Shuji
 ; APPLICANT: ISHIZAWA, Kenya
 ; TITLE OF INVENTION: STAT6 Activating Gene
 ; FILE REFERENCE: 1254-0207P
 ; CURRENT APPLICATION NUMBER: US/10/153,668
 ; CURRENT FILING DATE: 2002-05-24
 ; PRIOR APPLICATION NUMBER: US 60/293,172

; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: US 60/316,031
 ; PRIOR FILING DATE: 2001-08-31
 ; PRIOR APPLICATION NUMBER: US 60/328,403
 ; PRIOR FILING DATE: 2001-10-12
 ; PRIOR APPLICATION NUMBER: JP 2001-157043
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: JP 2001-260681
 ; PRIOR FILING DATE: 2001-08-30
 ; PRIOR APPLICATION NUMBER: JP 2001-313175
 ; PRIOR FILING DATE: 2001-10-10
 ; NUMBER OF SEQ ID NOS: 488
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 319
 ; LENGTH: 2113
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (138)..(1583)
 US-10-153-668-319

Query Match 62.1%; Score 23.6; DB 15; Length 2113;
 Best Local Similarity 76.3%; Pred. No. 41;
 Matches 29; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CAAAACTAGGTCAAAGGTCAAACTAGGTCAAAGGTCA 38
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 Db 1764 CACATCAGCATCAAAAGGTCAACACAAAGGTCAAGGTGA 1727
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RESULT 9

US-10-264-049-778/c

; Sequence 778, Application US/10264049
 ; Publication No. US20040005579A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Birse et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PAL3P1
 ; CURRENT APPLICATION NUMBER: US/10/264,049
 ; CURRENT FILING DATE: 2002-10-04
 ; PRIOR APPLICATION NUMBER: PCT/US01/18569
 ; PRIOR FILING DATE: 2001-06-07
 ; PRIOR APPLICATION NUMBER: US 60/209,467
 ; PRIOR FILING DATE: 2000-06-07
 ; NUMBER OF SEQ ID NOS: 4360
 ; SOFTWARE: PatentIn Ver. 3.1
 ; SEQ ID NO 778
 ; LENGTH: 2886
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (110)..(110)
 ; OTHER INFORMATION: n equals a,t,g, or c
 US-10-264-049-778

Query Match 62.1%; Score 23.6; DB 16; Length 2886;
 Best Local Similarity 76.3%; Pred. No. 44;
 Matches 29; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CAAAACTAGGTCAAAGGTCAAACTAGGTCAAAGGTCA 38
 |||||
 Db 926 CACATCAGCATCAAAAGGTCAACACAAAGGTCAAGGTCA 889
 |||||

RESULT 10

US-10-094-749-46/c

; Sequence 46, Application US/10094749
 ; Publication No. US20030219741A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ISOGAI, TAKAO
 ; APPLICANT: SUGIYAMA, TOMOYASU

Db 298 AAAACATGTTCAAAGTCAAACTATGTCT

Db 298 AAAACATGTTCAAAGTCAAACTATGTCT

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; SEQ ID NO 17516
; LENGTH: 467

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; SEQ ID NO 17516
; LENGTH: 467

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; TYPE: DNA
; ORGANISM: Human
US-10-027-632-17516

Query Match      56.8%; Score 21.6; DB 16; Length 467;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 27; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 AAAAAGTCTCAAAAGTCAAAAGTCAAAAGTCAAAAGTCA 37
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 264 AAATTAATCTCAAGGTAAAGGCAAGGCAATGAC 299

RESULT 14
US-10-437-963-27118/c
; Sequence 27118, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 27118
; LENGTH: 1161
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_31843C.1
US-10-437-963-27118

Query Match      56.8%; Score 21.6; DB 17; Length 1161;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 11 TCAAAGGTCAAAAGTCAAAAGTCAAAAGTCA 38
   ||||| ||||| ||||| ||||| ||||| |||||
DB 1037 TCAAATGTCAAATCTTGGTCAATGGTCA 1010

RESULT 15
US-10-302-172-879
; Sequence 879, Application US/10302172
; Publication No. US20040053250A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20040053250A1el Arginine-rich Protein-like Nucleic Acids ar
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803.1CNCP
; CURRENT APPLICATION NUMBER: US/10/302,172
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/225,251
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: PCT US02/05095
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/799,451
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 950
; SOFTWARE: Pf_FL_genes Version 2.0
; SEQ ID NO 879
; LENGTH: 2506
; TYPE: DNA
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (481)..(2154)
US-10-302-172-879

Query Match      56.8%; Score 21.6; DB 13; Length 2506;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 27; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 3 AAACTAGGTCAAAAGTCAAAAGTCAAAAGTCAAAAGTCA 38
   ||||| ||||| ||||| ||||| ||||| |||||
DB 794 AAACCAAGTCAAGGCCATGCTATGCTAGGTCA 829

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Job time : 37.8587 secs
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GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 08:16:17 ; Search time 5.97527 Seconds
(without alignments)
3529.238 Million cell updates/sec

Title: US-09-808-388-2

Perfect score: 38

Sequence: 1 caaaactaggctcaaaaggtcaaaactaggctcaaaaggtca 38

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	22	57.9	5910	1	US-08-135-814-1
C 2	22	57.9	5910	1	US-08-135-814-1
3	20.6	54.2	10953	4	US-08-956-171E-62
C 4	20.4	53.7	421	4	US-09-621-976-12838
5	20.4	53.7	3539	4	US-09-245-248B-59
6	20.4	53.7	3853	4	US-09-245-248B-53
7	20.4	53.7	4797	4	US-09-419-568F-25
8	20.4	53.7	4797	4	US-09-334-243B-25
9	20.2	53.2	11443	4	US-08-961-527-49
10	20	52.6	47	4	US-09-422-978-3108
11	19.8	52.1	786431	4	US-09-751-389-3
12	19.6	51.6	328	4	US-09-621-976-9939
C 13	19.6	51.6	2991	3	US-08-795-430-48
C 14	19.6	51.6	2991	4	US-09-355-700-48
15	19.6	51.6	3083	4	US-09-976-594-1022
16	19.6	51.6	66986	4	US-09-596-002-29
17	19.6	51.6	148567	4	US-09-801-876B-3
18	19.6	51.6	148567	4	US-10-254-869-3
C 19	19.6	51.6	152331	3	US-09-128-155-16
20	19.6	51.6	176373	3	US-09-128-155-17
21	19.4	51.1	321	1	US-08-322-742-11
22	19.4	51.1	478	4	US-09-023-655-1233
23	19.4	51.1	571	1	US-08-322-742-14
C 24	19.4	51.1	861	4	US-09-540-236-1011
25	19.4	51.1	2309	4	US-09-016-434-1249
26	19.4	51.1	3592	3	US-08-714-918-63
27	19.4	51.1	3592	3	US-09-265-315-63

28 19.4 51.1 3592 3 US-09-265-315-63 Sequence 63, Appl
29 19.4 51.1 3592 3 US-09-266-417-63 Sequence 63, Appl
30 19.4 51.1 3592 4 US-09-528-709-63 Sequence 63, Appl
31 19.4 51.1 3592 4 US-09-527-745-63 Sequence 63, Appl
32 19.4 51.1 6464 1 US-08-321-478-2 Sequence 2, Appl
33 19.4 51.1 6464 1 US-08-321-478-4 Sequence 4, Appl
34 19.4 51.1 269223 4 US-09-596-002-41 Sequence 6, Appl
C 35 19.4 51.1 269223 4 US-09-866-108A-15751 Sequence 41, Appl
C 36 19 50.0 1288 4 US-09-724-864-16 Sequence 15751, A
37 19 50.0 1288 4 US-09-336-536-37 Sequence 16, Appl
38 19 50.0 1288 4 US-08-956-171E-730 Sequence 37, Appl
C 39 18.8 49.5 481 4 US-08-956-171E-730 Sequence 730, App
C 40 18.8 49.5 1233 4 US-09-489-039A-2858 Sequence 2858, Ap
41 18.8 49.5 1380 4 US-09-489-039A-2858 Sequence 2890, Ap
42 18.8 49.5 2403 1 US-08-454-720A-41 Sequence 41, Appl
43 18.8 49.5 3061 2 US-08-692-787-47 Sequence 47, Appl
44 18.8 49.5 3061 3 US-09-097-199-47 Sequence 47, Appl
45 18.8 49.5 3537 4 US-09-245-248B-58 Sequence 58, Appl

ALIGNMENTS

RESULT 1

US-08-195-814-1
; Sequence 1, Application US/08195814
; Patent No. 5547869
; GENERAL INFORMATION:
; APPLICANT: DUMAS, BRUNO; GERVASIS, MONICA;
; APPLICANT: BERGION MAX; JOURDAN, MIREITTE; JOUSSET,
; APPLICANT: FRANCOISE XAVIERE
; TITLE OF INVENTION: NOVEL PLASMIDS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN AND MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/195,814
; FILING DATE: 14-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/881,054
; FILING DATE: 11-MAY-1992
; APPLICATION NUMBER: 07/278,735
; FILING DATE: 2-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 146.1029-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5910
; TYPE: NUCLEIC ACID
; STRANDEDNESS: UNKNOWN
; TOPOLOGY: UNKNOWN
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: DENSOVIRUS
; STRAIN: DENSOVIRUS OF JUNONIA
; INDIVIDUAL ISOLATE:

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1 STRANDEDNESS: UNKNOWN
2 TOPOLOGY: UNKNOWN
3 MOLECULE TYPE: CDNA
4 HYPOTHETICAL: NO
5 ORIGINAL SOURCE:
6 ORGANISM: DENSOVIRUS
7 STRAIN: DENSOVIRUS OF JUNONIA
8 INDIVIDUAL ISOLATE:
9 DEVELOPMENTAL STAGE: LARVAE
10 HAPLOTYPE:
11 TISSUE TYPE:
12 CELL TYPE: SPODOPTERA LITTORALIS
13 CELL LINE:
14 ORGANELLE:
15 FEATURE:
16 LOCATION: 1
17 OTHER INFORMATION: N IS A OR C OR G OR T,
18 OTHER INFORMATION: WHEREIN N IS ZERO TO 50 NUCLEOTIDES IN LENGTH
19 FEATURE:
20 LOCATION: 1657
21 OTHER INFORMATION: M IS A OR C
22 FEATURE:
23 LOCATION: 5619
24 OTHER INFORMATION: Y IS C OR T
25 FEATURE:
26 LOCATION: 5910
27 OTHER INFORMATION: N IS A OR C OR G OR T,
28 OTHER INFORMATION: WHEREIN N IS ZERO TO 130 NUCLEOTIDES IN LENGTH
29 US-08-195-814-1
30
31 Query Match 57.9%; Score 22; DB 1; Length 5910;
32 Best Local Similarity 73.7%; Pred. No. 12;
33 Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps
34
35 QY 1 CAAACCTAGGTCAAAGGTCAAACCTAGGTCAAAGGTCA 38
36 DB 195 CAGAAGTAGGTCAAAGGTCAATAGAGGTCAAAGGTCA 158
37
38 RESULT 3
39 US-08-956-171E-62
40 ; Sequence 62, Application US/08956171E
41 ; Patent No. 6593114
42 ; GENERAL INFORMATION:
43 ; APPLICANT: Charles Kunsch
44 ; Gil H. Choi
45 ; Patrick S. Dillon
46 ; Craig A. Rosen
47 ; Steven C. Barash
48 ; Michael R. Fannon
49 ; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and S
50 ; NUMBER OF SEQUENCES: 5256
51 ; CORRESPONDENCE ADDRESS:
52 ; ADDRESSEE: Human Genome Sciences, Inc.
53 ; STREET: 9410 Key West Avenue
54 ; CITY: Rockville
55 ; STATE: Maryland
56 ; COUNTRY: USA
57 ; ZIP: 20850
58 ; COMPUTER READABLE FORM:
59 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
60 ; COMPUTER: HP Vectra 486/33
61 ; OPERATING SYSTEM: MSDOS version 6.2
62 ; SOFTWARE: ASCII Text
63 ; CURRENT APPLICATION DATA:
64 ; APPLICATION NUMBER: US/08/956,171E
65 ; FILING DATE: 20-Oct-1997
66 ; CLASSIFICATION: <Unknown>
67 ; PRIOR APPLICATION DATA:
68 ; APPLICATION NUMBER: 60/009,861
69 ; FILING DATE: January 5, 1996
70 ; APPLICATION NUMBER: 08/781,986
71 ; FILING DATE: January 3, 1997

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; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 3539
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-245-248B-59

Query Match      53.7%; Score 20.4; DB 4; Length 3539;
Best Local Similarity 80.0%; Pred. No. 44;
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 9 GGTCAAAGGTCAAAACTAGGTCAAAGGTCA 38
Db 3462 GGTCAAAGGTCAAGCCTACGTACATAAGTCA 3491

RESULT 6
US-09-245-248B-53
; Sequence 53, Application US/09245248B
; Patent No. 6395472
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Leary, Thomas
; APPLICANT: Erker, James
; APPLICANT: Chalmers, Michelle
; APPLICANT: Simons, John
; APPLICANT: Birkenmeyer, Larry
; APPLICANT: Muerhoff, Scott
; APPLICANT: Pilot-Macias, Tami
; APPLICANT: Desai, Suresh
; APPLICANT: Mushahwar, Isa
; TITLE OF INVENTION: METHODS OF UTILIZING THE TT VIRUS
; FILE REFERENCE: 6461.US.01
; CURRENT APPLICATION NUMBER: US/09/245,248B
; CURRENT FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 3853
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-245-248B-53

Query Match      53.7%; Score 20.4; DB 4; Length 3853;
Best Local Similarity 80.0%; Pred. No. 44;
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 9 GGTCAAAGGTCAAAACTAGGTCAAAGGTCA 38
Db 3568 GGTCAAAGGTCACTGCTACGTATAGTCA 3597

RESULT 7
US-09-419-568F-25
; Sequence 25, Application US/09419568F
; Patent No. 6331613
; GENERAL INFORMATION:
; APPLICANT: Dumoutier, Laure
; APPLICANT: Louhed, Jamila
; APPLICANT: Renauld, Jean-Christophe
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Induc
; TITLE OF INVENTION: (TIFs) The Proteins Encoded, and Uses Thereof
; FILE REFERENCE: LUD 543.2
; CURRENT APPLICATION NUMBER: US/09/419,568F
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US09/354,243
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US09/178,973
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 25
; LENGTH: 4797

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-419-568F-25

Query Match      53.7%; Score 20.4; DB 4; Length 4797;
Best Local Similarity 80.0%; Pred. No. 46;
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 AAAAAGTCAAGTCAAAAGTCAAAAGTCAAGTCA 31
Db 1788 AAATCTAGTCACTGTTGAAATCTAGTCA 1817

RESULT 8
US-09-354-243B-25
; Sequence 25, Application US/09354243B
; Patent No. 6359117
; GENERAL INFORMATION:
; APPLICANT: Dumoutier, Laure
; APPLICANT: Louhed, Jamila
; APPLICANT: Renauld, Jean-Christophe
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Peptides
; TITLE OF INVENTION: (TIPs)
; TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
; FILE REFERENCE: LUD 5543.1
; CURRENT APPLICATION NUMBER: US/09/354,243B
; CURRENT FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US09/178,973
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 25
; LENGTH: 4797
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-354-243B-25

Query Match      53.7%; Score 20.4; DB 4; Length 4797;
Best Local Similarity 80.0%; Pred. No. 46;
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 AAAAAGTCAAGTCAAAAGTCAAAAGTCAAGTCA 31
Db 1788 AAATCTAGTCACTGTTGAAATCTAGTCA 1817

RESULT 9
US-09-961-527-49
; Sequence 49, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11443 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-49

Query Match      53.2%; Score 20.2; DB 4; Length 11443;
Best Local Similarity 75.8%; Pred. No. 66;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4 AACTAGTCAAAAGTCAAAAGTCAAAAGTCAAAAGT 36
Db 6901 AAAAGTCAAAAGTCAAAAGTCAAAAGTCAAAAGT 6933

RESULT 10
US-09-422-978-3108
; Sequence 3108, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 3108
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-23549-78 : polymorphic base G or A
US-09-422-978-3108

Query Match      52.6%; Score 20; DB 4; Length 47;
Best Local Similarity 76.7%; Pred. No. 26;
Matches 23; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 7 TAGTCAAGTCAAAAGTCAAAAGTCAAAAGT 36
Db 17 TAGTCCRAAGTCAAAATTAGGTAAAGAT 46

RESULT 11
US-09-751-389-3
; Sequence 3, Application US/09751389
; Patent No. 6630334
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES THEREOF
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001067
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; CURRENT APPLICATION NUMBER: US/09/751,389
; CURRENT FILING DATE: 2001-01-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 786431
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(786431)
; OTHER INFORMATION: n = A,T,C or G
US-09-751-389-3

Query Match 52.1%; Score 19.8; DB 4; Length 786431;
Best Local Similarity 77.4%; Pred. No. 1.9e+02;
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 AAAGTAGTCAAGGTCAAAGCTAGGTCAA 33
Db 190533 AAAATAGGTTAAAGGCAACCTACTTGAA 190563

RESULT 12

US-09-621-976-9939
; Sequence 9939, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 9939
; LENGTH: 328
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-9939

Query Match 51.6%; Score 19.6; DB 4; Length 328;
Best Local Similarity 73.5%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 5 ACTAGGTCAAGGTCAAAGCTAGGTCAAAGGTCA 38
Db 15 AGTATGACCATGGTTGAACCAAGGTCAAAGGTGA 48

RESULT 13

US-08-795-430-48/c
; Sequence 48, Application US/08795430
; Patent No. 6130071
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Joukov, Vladimir
; TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
; TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,430
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FI96/00427
; FILING DATE: 01-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/671,573
; FILING DATE: 28-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/601,132
; FILING DATE: 14-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585,895
; FILING DATE: 12-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/510,133
; FILING DATE: 01-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/340,011
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28967/33691
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2991 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-795-430-48

Query Match 51.6%; Score 19.6; DB 3; Length 2991;
Best Local Similarity 73.5%; Pred. No. 85;
Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CAAAGTAGTCAAGGTCAAAGCTAGGTCAAAG 34
Db 1968 CAAAGTTGGAAAAGGTCATCATGTGTGAG 1935

RESULT 14

US-09-355-700-48/c
; Sequence 48, Application US/09355700
; Patent No. 6361946
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research
; Helsinki University Licensing
; Alitalo, Kari (U.S. only)
; Joukov, Vladimir (U.S. only)
; TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

Search completed: September 11, 2004, 09:33:11
Job time : 7.97527 secs

Query Match	51.6%;	Score 19.6;	DB 4;	Length 3083;
Best Local Similarity	73.5%;	Pred. No. 86;		
25. Conservative	0;	Mismatches	9;	Indels 0;
Gaps	0;			

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 07:30:11 : Search time 468 Seconds

(without alignments)

1881.445 Million cell updates/sec

Title: US-09-808-388-5_COPY_1_175

Perfect score: 175

Sequence: 1 cgcggcaaaactgctgaaa.....tccccagccttgctgcctcac 175

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 6608766

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
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8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
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10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
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13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
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18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	175	100.0	271	9	US-09-808-388-5
2	175	100.0	332	9	US-09-808-388-5
3	128	73.1	1080	10	US-09-865-866-17
C 4	110.8	63.3	6083	13	US-10-221-714A-440
5	94.8	54.2	6083	13	US-10-221-714A-439
6	47	26.9	3330	9	US-09-917-800A-1495
7	47	26.9	3330	12	US-10-152-319A-2157
8	47	26.9	3330	16	US-10-191-803-398
9	44.4	25.4	4990	10	US-09-865-866-97
C 10	34.2	19.5	371	15	US-10-387-495-8
11	32.6	18.6	54552	13	US-10-087-192-1303
12	32.4	18.5	819	13	US-10-027-632-130312
13	32.4	18.5	819	16	US-10-027-632-130312
14	32.2	18.4	573	13	US-10-027-632-50048

15	32.2	18.4	573	13	US-10-027-632-50049	Sequence 50049, A
16	32.2	18.4	573	13	US-10-027-632-69880	Sequence 69880, A
17	32.2	18.4	573	13	US-10-027-632-69881	Sequence 69881, A
18	32.2	18.4	573	13	US-10-027-632-70565	Sequence 70565, A
19	32.2	18.4	573	13	US-10-027-632-70566	Sequence 70566, A
20	32.2	18.4	573	13	US-10-027-632-70565	Sequence 70565, A
21	32.2	18.4	573	16	US-10-027-632-50048	Sequence 50048, A
22	32.2	18.4	573	16	US-10-027-632-50049	Sequence 50049, A
23	32.2	18.4	573	16	US-10-027-632-69880	Sequence 69880, A
24	32.2	18.4	573	16	US-10-027-632-69881	Sequence 69881, A
25	32.2	18.4	573	16	US-10-027-632-70565	Sequence 70565, A
26	31.2	17.8	420	15	US-10-027-632-70566	Sequence 70566, A
27	31.2	17.8	1441	15	US-10-422-264-17	Sequence 17, Appl
28	31.2	17.8	2136	9	US-09-862-658-13	Sequence 13, Appl
29	31.2	17.8	2136	15	US-10-175-696-24	Sequence 24, Appl
30	31.2	17.8	2136	17	US-10-776-871-24	Sequence 24, Appl
31	31.2	17.8	2236	15	US-10-422-264-5	Sequence 5, Appl
32	31.2	17.8	2307	13	US-10-302-172-803	Sequence 23, Appl
33	31.2	17.8	2604	15	US-10-422-264-23	Sequence 1, Appl
34	31.2	17.8	2701	15	US-10-422-264-1	Sequence 1, Appl
35	31.2	17.8	3320	9	US-09-862-658-1	Sequence 22, Appl
36	31.2	17.8	3320	15	US-10-175-696-22	Sequence 22, Appl
37	31.2	17.8	3320	17	US-10-776-871-22	Sequence 29, Appl
38	31.2	17.8	3384	15	US-10-422-264-29	Sequence 1474, Ap
39	30.6	17.5	250	15	US-10-066-543-1474	Sequence 618, App
C 40	30.6	17.5	305	9	US-09-879-536-618	Sequence 43, Appl
C 41	30.6	17.5	2856	13	US-10-231-956A-43	Sequence 7, Appl
C 42	30.6	17.5	2856	16	US-10-373-801-7	Sequence 3388, Ap
C 43	30.6	17.5	2885	9	US-09-880-107-3388	Sequence 245, App
C 44	30.6	17.5	2885	13	US-10-262-511-245	Sequence 351, App
C 45	30.6	17.5	2885	13	US-10-307-817-351	

ALIGNMENTS

RESULT 1

US-09-808-388-5
; Sequence 5, Application US/09808388
; Patent No. US20020081719A1
; GENERAL INFORMATION:
; APPLICANT: Massaad, Charbel
; APPLICANT: Berenbaum, Francis
; APPLICANT: Olivier, Jean-Luc
; APPLICANT: Salvat, Colette
; APPLICANT: Berezziat, Gilbert
; TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising them
; FILE OF INVENTION: their uses
; FILE REFERENCE: ST00010
; CURRENT APPLICATION NUMBER: US/09/808,388
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: FR/00/03262
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/196,959
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 271
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fragment of the PLA2s promoter
US-09-808-388-5

Query Match 100.0%; Score 175; DB 9; Length 271;

Best Local Similarity 100.0%; Pred. No. 2.6e-54;

Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGCGCAAAACTGCCGAAATGTTTGGCATCAGTACTGACAGTAAAGTTTCCCAA 60

1 CGCGCAAAACTGCCGAAATGTTTGGCATCAGTACTGACAGTAAAGTTTCCCAA 60

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QY 61 TCCTCAACTGTCTGCTCCAGCTGATGAGGGGAAGAAAGGATTAACCTAGGGGTATGGG 120
Db 61 TCCTCAACTGTCTGCTCCAGCTGATGAGGGGAAGAAAGGATTAACCTAGGGGTATGGG 120

QY 121 CGACCAATCCTGAGTCCACCACTGACACCGCCCATCCCGAGCTTGTGCTCTCAC 175
Db 121 CGACCAATCCTGAGTCCACCACTGACACCGCCCATCCCGAGCTTGTGCTCTCAC 175

RESULT 2
US-09-808-388-6
; Sequence 6, Application US/09808388
; Patent No. US20020081719A1
; GENERAL INFORMATION:
; APPLICANT: Massaad, Charbel
; APPLICANT: Berenbaum, Francis
; APPLICANT: Olivier, Jean-Luc
; APPLICANT: Salvat, Colette
; APPLICANT: Berezat, Gilbert
; TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising them
; TITLE OF INVENTION: their uses
; FILE REFERENCE: ST00010
; CURRENT APPLICATION NUMBER: US/09/808,388
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: FR/00/03262
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/196,959
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6
; LENGTH: 332
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PPRE/PLA2s hybrid promoter
US-09-808-388-6

Query Match 100.0%; Score 175; DB 9; Length 332;
Best Local Similarity 100.0%; Pred. No. 2.8e-54;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCAAACTGCTGAAATGTGTTTGGCATCAGCTACTGACAGTAAAGTTTCCCAA 60
Db 62 CGCGCAAACTGCTGAAATGTGTTTGGCATCAGCTACTGACAGTAAAGTTTCCCAA 121

QY 61 TCCTCAACTGTCTGCTCCAGCTGATGAGGGGAAGAAAGGATTAACCTAGGGGTATGGG 120
Db 122 TCCTCAACTGTCTGCTCCAGCTGATGAGGGGAAGAAAGGATTAACCTAGGGGTATGGG 181

QY 121 CGACCAATCCTGAGTCCACCACTGACACCGCCCATCCCGAGCTTGTGCTCTCAC 175
Db 182 CGACCAATCCTGAGTCCACCACTGACACCGCCCATCCCGAGCTTGTGCTCTCAC 236

RESULT 3
US-09-865-866-17
; Sequence 17, Application US/09865866
; Publication No. US20030045487A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
; FILE REFERENCE: RTS-0221
; CURRENT APPLICATION NUMBER: US/09/865,866
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 17
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-865-866-17
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Query Match 73.1%; Score 128; DB 10; Length 1080;
Best Local Similarity 89.9%; Pred. No. 1.1e-36;
Matches 160; Conservative 0; Mismatches 15; Indels 3; Gaps 2;

QY 1 CGCGCAAACTGCTGAAATGTGTTTGGCATCAGCTACTGACACGTAA-GGTTTCCCA 59
Db 763 CTCGGCAAACTGCTGAAATGTGTTTGGCATCAGCTACTGACACGTAAAGGTTTCCCA 822

QY 60 ATCCTCAACTGTGCTCTG--CCAGCTGATAGGGGAAGAAAGGATTAACCTAGGGGTAT 117
Db 823 ATCCTCAACTGTGCTCTGCGCCAGGCTGATGAGGGGAAGAAAGGATTAACCTAGGGGTAT 882

QY 118 GGGCGACCAATCCTGAGTCCACCACTGACACGCCCCATCCCCAGCCTTGTGCTCTCAC 175
Db 883 GGGCGACCAATCCTGAGTCCACCACTGACACGCCCCATCCCCAGCCTTGTGCTCTCAC 940

RESULT 4
US-10-221-714A-440/c
; Sequence 440, Application US/10221714A
; Publication No. US20040048254A1
; GENERAL INFORMATION:
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; TITLE OF INVENTION: tumor suppressor genes and oncogenes
; FILE REFERENCE: 5013.1005
; CURRENT APPLICATION NUMBER: US/10/221,714A
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: PCT/EP01/02955
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: DE 10013847.0
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 540
; SEQ ID NO 440
; LENGTH: 6083
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-221-714A-440

Query Match 63.3%; Score 110.8; DB 13; Length 6083;
Best Local Similarity 78.2%; Pred. No. 4.5e-30;
Matches 133; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 6 CAAAACCTGCTGAAATGTGTTTGGCATCAGCTACTGACACGTAAAGTTTCCCAATCCTC 65
Db 1324 CAAAACCTGCTGAAATGTGTTTGGCATCAGCTACTGACACGTAAATTTCCCAATCCTC 1265

QY 66 AACTCTGCTGCTGAGTGGGGAAGAAAGGATTAACCTAGGGGTATGGGGGACC 125
Db 1264 AACTCTATCTTACCACCTAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 1205

QY 126 AATCTGAGTCCACCACTGACACGCCCCATCCCCAGCCTTGTGCTCTCAC 175
Db 1204 AATCTAAATCCACCACTAATACCAACGCCCCATCCCCAACCTTATACCTCTCAC 1155

RESULT 5
US-10-221-714A-439
; Sequence 439, Application US/10221714A
; Publication No. US20040048254A1
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GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with
TITLE OF INVENTION: tumor suppressor genes and oncogenes
FILE REFERENCE: 5013.1005
CURRENT APPLICATION NUMBER: US/10/221.714A
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: PCT/EP01/02955
PRIOR FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: DE 10013847.0
PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 540
SEQ ID NO 439
LENGTH: 6083
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-221-714A-439

Query Match 54.2%; Score 94.8; DB 13; Length 6083;
Best Local Similarity 72.4%; Pred. No. 3.8e-24;
Matches 123; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 5 CAAAACCTGCTGAAATGCTTTGGCATCGCTACTACACAGTAAGGTTTCCCAATCCT 64
Db 4759 GTAAATGTTTGAATGCTTTGGTATTGTTATGATAGTAAGGTTTTHAATTT 4818
Qy 65 CAACCTCTCTGCGCAGCTGATGAGGGAAGAAAGGATACCTAGGGGTATGGCGAC 124
Db 4819 TAAATTTGTTTGTAGTTGATGAGGGAAGAAAGGATATTTAGGGGTATGGCGAT 4878
Qy 125 CAATCCTGAGTCCACCACTACACAGCCCATCCCGAGCTTGCCCTCA 174
Db 4879 TAAATTTGAGTTTATTAATGATTAGTTTATTTAGTTTGTGTTTA 4928

RESULT 6
US-09-917-800A-1495
Sequence 1495, Application US/09917800A
Patent No. US20020119462A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295,798

PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1495
LENGTH: 3330
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020119462A1 X51529
US-09-917-800A-1495

Query Match 26.9%; Score 47; DB 9; Length 3330;
Best Local Similarity 60.5%; Pred. No. 1.5e-06;
Matches 95; Conservative 0; Mismatches 60; Indels 2; Gaps 1;
Qy 6 CAAAACCTGCTGAAATGCTTTGGCATCGCTACTACACAGTAAGGTTTCCCAATCCTC 65
Db 260 CGAAATCAGCTAAAGTTTATGATGCCACACACCCATGCTATGAGGGCTTTTCCGGCCCTC 319
Qy 66 AACTCTCTCTGCCAGCTGATGAGGGAAGAAAGGATACCTAGGGGTATGGG--CGA 123
Db 320 AAGCTTGTTCGCCAGCTGTTGGGGGGAAGAAAGGGAATTAACCCAGGGCGTTGGTATGC 379
Qy 124 CCAATCCTGAGTCCACCACTGACACGCCCATCCCC 160
Db 380 CCGTCTGTGAATCCATTATTTGGCCACACCCACCTCC 416

RESULT 7
US-10-152-319A-2157
Sequence 2157, Application US/10152319A
Publication No. US20040072160A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Higgs, Brandon
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5089-US
CURRENT APPLICATION NUMBER: US/10/152,319A
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: US 60/292,335
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/297,523
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,925
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,810
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/303,807
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/303,808
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/315,047
PRIOR FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: US 60/324,928
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US 60/330,867
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: US 60/330,462
PRIOR FILING DATE: 2001-10-22
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2221
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2157

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/ LENGTH: 3330
/ TYPE: DNA
/ ORGANISM: Rattus norvegicus
/ FEATURE:
/ OTHER INFORMATION: Genbank Accession No. X51529
US-10-152-319A-2157

Query Match      26.9%; Score 47; DB 12; Length 3330;
Best Local Similarity 60.5%; Pred. No. 1.5e-06;
Matches 95; Conservative 0; Mismatches 60; Indels 2; Gaps 1;

QY 6 CAAAACTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAATCCTC 65
Db 260 CGAAATCAGCTAAAGTTTATGATGGCCACACCAATGATGAGGGCTTTTCGGCCCTC 319

QY 66 AACTCTGTCTGCCAGCTGATGAGGGGAAGAAAGGATTAACCTAGGGGTATGGG--CGA 123
Db 320 AAGGCTGTCTGCCAGCTGTGAGGGGAAAGGGGAAATTAACCCAGGGCGTTGGGTATGC 379

QY 124 CCAATCCTGAGTCCACCACTGACACCGCCCATCCCC 160
Db 380 CCGTCTGTGAATCAATTTTGGCCACACCCACTCC 416

RESULT 8
US-10-191-803-398
/ Sequence 398, Application US/10191803
/ Publication No. US20040014040A1
/ GENERAL INFORMATION:
/ APPLICANT: MENDRICK, Donna
/ APPLICANT: PORTER, Mark
/ APPLICANT: JOHNSON, Kory
/ APPLICANT: HIGGS, Brandon
/ APPLICANT: CASTLE, Arthur
/ APPLICANT: ELASHOFF, Michael
/ TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
/ FILE REFERENCE: 44921-5090US
/ CURRENT APPLICATION NUMBER: US/10/191,803
/ CURRENT FILING DATE: 2002-07-10
/ PRIOR APPLICATION NUMBER: US 60/303,819
/ PRIOR FILING DATE: 2001-07-10
/ PRIOR APPLICATION NUMBER: US 60/305,623
/ PRIOR FILING DATE: 2001-07-17
/ PRIOR APPLICATION NUMBER: US 60/369,351
/ PRIOR FILING DATE: 2002-04-03
/ PRIOR APPLICATION NUMBER: US 60/377,611
/ PRIOR FILING DATE: 2002-05-06
/ NUMBER OF SEQ ID NOS: 1140
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 398
/ LENGTH: 3330
/ TYPE: DNA
/ ORGANISM: Rattus norvegicus
/ FEATURE:
/ OTHER INFORMATION: Genbank Accession No. US20040014040A1 X51529
US-10-191-803-398

Query Match      26.9%; Score 47; DB 16; Length 3330;
Best Local Similarity 60.5%; Pred. No. 1.5e-06;
Matches 95; Conservative 0; Mismatches 60; Indels 2; Gaps 1;

QY 6 CAAAACTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAATCCTC 65
Db 260 CGAAATCAGCTAAAGTTTATGATGGCCACACCAATGATGAGGGCTTTTCGGCCCTC 319

QY 66 AACTCTGTCTGCCAGCTGATGAGGGGAAGAAAGGATTAACCTAGGGGTATGGG--CGA 123
Db 320 AAGGCTGTCTGCCAGCTGTGAGGGGAAAGGGGAAATTAACCCAGGGCGTTGGGTATGC 379

QY 124 CCAATCCTGAGTCCACCACTGACACCGCCCATCCCC 160
Db 380 CCGTCTGTGAATCAATTTTGGCCACACCCACTCC 416
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RESULT 9
US-09-865-866-97
/ Sequence 97, Application US/09865866
/ Publication No. US20030045487A1
/ GENERAL INFORMATION:
/ APPLICANT: C. Frank Bennett
/ APPLICANT: Jacqueline Wyatt
/ TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL)
/ FILE REFERENCE: RTS-0221
/ CURRENT APPLICATION NUMBER: US/09/865,866
/ CURRENT FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 173
/ SEQ ID NO 97
/ LENGTH: 4990
/ TYPE: DNA
/ ORGANISM: Mus musculus
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (2026)...(2068)
/ NAME/KEY: CDS
/ LOCATION: (2245)...(2389)
/ NAME/KEY: CDS
/ LOCATION: (2622)...(2731)
/ NAME/KEY: CDS
/ LOCATION: (4098)...(4240)
US-09-865-866-97

Query Match      25.4%; Score 44.4; DB 10; Length 4990;
Best Local Similarity 61.0%; Pred. No. 1.6e-05;
Matches 72; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

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QY 66 AACTCTGTCTGCCAGCTGATGAGGGGAAGAAAGGATTAACCTAGGGGTATGGGGA 123
Db 1076 AGGGCTGCCCTGCCAGCTGTGGGGAAACAAAAGGCAATGGGTATGCCCATCCGTGA 1133

RESULT 10
US-10-387-495-8/c
/ Sequence 8, Application US/10387495
/ Publication No. US20030162956A1
/ GENERAL INFORMATION:
/ APPLICANT: Ni et al.
/ TITLE OF INVENTION: Leukocyte Regulatory Factors 1 and 2
/ FILE REFERENCE: PF359CI
/ CURRENT APPLICATION NUMBER: US/10/387,495
/ CURRENT FILING DATE: 2003-03-14
/ PRIOR APPLICATION NUMBER: US/09/603,735A
/ PRIOR FILING DATE: 2000-06-23
/ PRIOR APPLICATION NUMBER: 09/055,998
/ PRIOR FILING DATE: 1998-04-07
/ PRIOR APPLICATION NUMBER: 60/043,483
/ PRIOR FILING DATE: 1997-04-07
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 8
/ LENGTH: 371
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-387-495-8

Query Match      19.5%; Score 34.2; DB 15; Length 371;
Best Local Similarity 51.7%; Pred. No. 0.039; 73; Indels 0; Gaps 0;
Matches 78; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 23 TGTTTTGGCATCAGTACTGACGTAAGGTTTCCCAATCCTCAACTCTGTCTGCCAGC 82
Db 238 TGTGTGGGCAACAGCCGCCAGGCTAGGAGTCCCTCCCTCAAAATCTCTCCACCC 179
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Mon Sep 13 07:48:10 2004

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; SEQ ID NO 50049
; LENGTH: 573
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-50049

Query Match      18.4%; Score 32.2; DB 13; Length 573;
Best Local Similarity 53.6%; Pred. No. 0.25;
Matches 67; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

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Db      283 GGGGTAAACAGCTGTTATGTCTCCCAAAAACAGAAATCTCCCATCCATAATGCACAACCTGC 342
Qy      161 AGCCT 165
Db      343 AGCCT 347

Search completed: September 11, 2004, 09:28:32
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GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: 2002-04-30
; PRIORITY APPLICATION NUMBER: US 60/218,006
; PRIORITY FILING DATE: 2000-07-12
; PRIORITY APPLICATION NUMBER: US 60/198,676
; PRIORITY FILING DATE: 2000-04-20
; PRIORITY APPLICATION NUMBER: US 60/193,483
; PRIORITY FILING DATE: 2000-03-29
; PRIORITY APPLICATION NUMBER: US 60/185,218
; PRIORITY FILING DATE: 2000-02-24
; PRIORITY APPLICATION NUMBER: US 60/167,363
; PRIORITY FILING DATE: 1999-11-23
; PRIORITY APPLICATION NUMBER: US 60/156,358
; PRIORITY FILING DATE: 1999-09-28
; PRIORITY APPLICATION NUMBER: US 60/146,002
; PRIORITY FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50048
; LENGTH: 573
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-50048

Query Match      18.4%; Score 32.2; DB 13; Length 573;
Best Local Similarity 53.6%; Pred. No. 0.25;
Matches 67; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

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Db      223 TGACACAGAGGGTCTTCAAGAGCAAACTAGTCATTTCAGACTATAGTTGAGTAAGAACA 282
Qy      101 GGATTACCTAGGGGTATGGCGACCAATCCTGAGTCCACCAACTGACACGCCCATCCCC 160
Db      283 GGGGTAAACAGCTGTTATGTCTCCCAAAAACAGAAATCTCCCATCCATAATGCACAACCTGC 342
Qy      161 AGCCT 165
Db      343 AGCCT 347

RESULT 15
US-10-027-632-50049
; Sequence 50049, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: 2002-04-30
; PRIORITY APPLICATION NUMBER: US 60/218,006
; PRIORITY FILING DATE: 2000-07-12
; PRIORITY APPLICATION NUMBER: US 60/198,676
; PRIORITY FILING DATE: 2000-04-20
; PRIORITY APPLICATION NUMBER: US 60/193,483
; PRIORITY FILING DATE: 2000-03-29
; PRIORITY APPLICATION NUMBER: US 60/185,218
; PRIORITY FILING DATE: 2000-02-24
; PRIORITY APPLICATION NUMBER: US 60/167,363
; PRIORITY FILING DATE: 1999-11-23
; PRIORITY APPLICATION NUMBER: US 60/156,358
; PRIORITY FILING DATE: 1999-09-28
; PRIORITY APPLICATION NUMBER: US 60/146,002
; PRIORITY FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0

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OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-09-808-388-1

Perfect score: 20

Sequence: 1 caaaactagggtcaagggtca 20

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 6608766

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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- 19: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	20	100.0	20	10	US-09-877-705A-67
3	20	100.0	20	10	US-09-877-705A-68
4	20	100.0	20	10	US-09-877-738A-67
5	20	100.0	20	10	US-09-877-738A-68
6	20	100.0	20	13	US-09-947-274-67
7	20	100.0	20	13	US-09-947-274-68
8	20	100.0	20	17	US-10-779-595-67
9	20	100.0	20	17	US-10-779-595-68
10	20	100.0	38	9	US-09-808-388-2
11	20	100.0	41	9	US-09-808-388-3
12	20	100.0	52	9	US-09-808-388-4
13	20	100.0	60	10	US-09-877-705A-142
14	20	100.0	60	10	US-09-877-738A-142

c	15	20	100.0	60	13	US-09-947-274-142	Sequence 142, App
c	16	20	100.0	60	17	US-10-779-595-142	Sequence 142, App
	17	20	100.0	332	9	US-09-808-388-6	Sequence 6, Appli
	18	18	90.0	18	13	US-10-366-715-9	Sequence 9, Appli
	19	17.4	87.0	118502	13	US-10-087-192-397	Sequence 397, App
	20	17	85.0	25	14	US-10-113-897-133	Sequence 72, Appl
c	21	16.8	84.0	506	10	US-09-764-891-72	Sequence 133, App
c	22	16.8	84.0	506	13	US-10-091-414-15	Sequence 15, Appl
c	23	16.8	84.0	2398	17	US-10-437-963-26314	Sequence 26314, A
c	24	16.8	84.0	74788	13	US-10-087-192-1906	Sequence 1906, Ap
c	25	16.4	82.0	18	13	US-10-366-715-11	Sequence 11, Appl
c	26	16.4	82.0	1857	13	US-10-424-599-121181	Sequence 121181,
c	27	16.4	82.0	2286	15	US-10-153-668-389	Sequence 389, App
c	28	16.4	82.0	2473	15	US-10-153-668-383	Sequence 383, App
c	29	16.4	82.0	2473	15	US-10-153-668-385	Sequence 385, App
c	30	16.4	82.0	2572	15	US-10-153-668-387	Sequence 387, App
c	31	16.4	82.0	2584	15	US-10-153-668-391	Sequence 391, App
c	32	16.4	82.0	4292	13	US-10-102-806-179	Sequence 179, App
c	33	16.4	82.0	4292	15	US-09-925-298-179	Sequence 271, App
c	34	16.4	82.0	5516	15	US-10-153-668-271	Sequence 14617, A
c	35	16	80.0	724	13	US-10-027-632-14617	Sequence 14617, A
	36	16	80.0	724	16	US-10-027-632-14617	Sequence 22, Appl
	37	15.8	79.0	31	16	US-10-238-960-22	Sequence 11556, A
c	38	15.8	79.0	659	13	US-10-027-632-11556	Sequence 11556, A
c	39	15.8	79.0	659	16	US-10-027-632-11556	Sequence 271, App
c	40	15.8	79.0	679	13	US-09-854-867-271	Sequence 13893, A
c	41	15.8	79.0	878	15	US-10-198-846-13893	Sequence 9, Appli
c	42	15.8	79.0	1269	13	US-10-210-281-11	Sequence 46204, A
c	43	15.8	79.0	1287	13	US-10-210-281-9	Sequence 97508, A
c	44	15.8	79.0	1437	16	US-10-369-493-46204	
c	45	15.8	79.0	1865	13	US-10-027-632-97508	

ALIGNMENTS

RESULT 1
US-09-808-388-1
; Sequence 1, Application US/09808388
; Patent No. US20020081719A1
; GENERAL INFORMATION:
; APPLICANT: Massaad, Charbel
; APPLICANT: Berenbaum, Francis
; APPLICANT: Olivier, Jean-Luc
; APPLICANT: Salvat, Colette
; APPLICANT: Berezat, Gilbert
; TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising them
; TITLE OF INVENTION: their uses
; FILE REFERENCE: ST00010
; CURRENT APPLICATION NUMBER: US/09/808,388
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: FR/00/03262
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/196,959
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PPSE element
US-09-808-388-1

Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAACCTAGGTCAAAGGTCA 20

Db 1 CAAAACCTAGGTCAAAGGTCA 20

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; SOFTWARE: Patentin version 3.1
; SEQ ID NO 67
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Transcription factor probe PP67
US-09-877-738A-67

Query Match      100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAACTAGGTCAAAGGTCA 20
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DB 1 CAAAACTAGGTCAAAGGTCA 20

RESULT 5
US-09-877-738A-68/c
; Sequence 68, Application US/09877738A
; Publication No. US20030022173A1
; GENERAL INFORMATION:
; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED
; FILE REFERENCE: 26757-701
; CURRENT APPLICATION NUMBER: US/09/877,738A
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 68
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Transcription factor probe PP68
US-09-877-738A-68

Query Match      100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAACTAGGTCAAAGGTCA 20
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DB 20 CAAAACTAGGTCAAAGGTCA 1

RESULT 6
US-09-947-274-67
; Sequence 67, Application US/09947274
; Publication No. US20030017499A1
; GENERAL INFORMATION:
; APPLICANT: Li, Xianqiang
; TITLE OF INVENTION: METHOD FOR DETECTING TRANSCRIPTION FACTOR-PROTEIN INTERACTIONS
; FILE REFERENCE: 26757-705
; CURRENT APPLICATION NUMBER: US/09/947,274
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 09/877,738
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/877,243
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/877,403
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/877,705
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 67
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:

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; SOFTWARE: Patentin version 3.1
; SEQ ID NO 67
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Transcription factor probe PP67
US-09-877-705A-67

Query Match      100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAACTAGGTCAAAGGTCA 20
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DB 1 CAAAACTAGGTCAAAGGTCA 20

RESULT 3
US-09-877-705A-68/c
; Sequence 68, Application US/09877705A
; Publication No. US20030008283A1
; GENERAL INFORMATION:
; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD FOR SCREENING FOR DRUG CANDIDATES FOR MODULATING TRANSCRIPTION FACTOR ACTIVITY
; FILE REFERENCE: 26757-704
; CURRENT APPLICATION NUMBER: US/09/877,705A
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 68
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Transcription factor probe PP68
US-09-877-705A-68

Query Match      100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 20 CAAAACTAGGTCAAAGGTCA 1

RESULT 4
US-09-877-738A-67
; Sequence 67, Application US/09877738A
; Publication No. US20030022173A1
; GENERAL INFORMATION:
; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED
; FILE REFERENCE: 26757-701
; CURRENT APPLICATION NUMBER: US/09/877,738A
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 162

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OTHER INFORMATION: Transcription factor probe PP67
US-09-947-274-67

Query Match 100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAACTAGGTCAAAGGTCA 20
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Db 1 CAAACTAGGTCAAAGGTCA 20

RESULT 7
US-09-947-274-68/c
; Sequence 68, Application US/09947274
; Publication No. US20030017499A1
; GENERAL INFORMATION:
; APPLICANT: Li, Xiangqiang
; TITLE OF INVENTION: METHOD FOR DETECTING TRANSCRIPTION FACTOR-PROTEIN INTERACTIONS
; FILE REFERENCE: 26757-705
; CURRENT APPLICATION NUMBER: US/09/947,274
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 09/877,738
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/877,243
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/877,403
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/877,705
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Transcription factor probe PP68
US-09-947-274-68

Query Match 100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAACTAGGTCAAAGGTCA 20
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Db 20 CAAACTAGGTCAAAGGTCA 1

RESULT 8
US-10-779-595-67
; Sequence 67, Application US/10779595
; Publication No. US20040132090A1
; GENERAL INFORMATION:
; APPLICANT: Li, Xiangqiang
; TITLE OF INVENTION: METHOD, ARRAY AND KIT FOR DETECTING ACTIVATED TRANSCRIPTION FACTOR
; FILE REFERENCE: 26757-702.301
; CURRENT APPLICATION NUMBER: US/10/779,595
; PRIOR FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: 09/877,243
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Transcription factor probe PP67
US-10-779-595-67

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CAAACTAGGTCAAAGGTCA 20

RESULT 9
US-10-779-595-68/c
; Sequence 68, Application US/10779595
; Publication No. US20040132090A1
; GENERAL INFORMATION:
; APPLICANT: Li, Xiangqiang
; TITLE OF INVENTION: METHOD, ARRAY AND KIT FOR DETECTING ACTIVATED TRANSCRIPTION FACTOR
; FILE REFERENCE: 26757-702.301
; CURRENT APPLICATION NUMBER: US/10/779,595
; PRIOR FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: 09/877,243
; PRIOR FILING DATE: 2001-06-08
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US-10-779-595-68

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Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 20 CAAACTAGGTCAAAGGTCA 1

RESULT 10
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; Patent No. US20020081719A1
; GENERAL INFORMATION:
; APPLICANT: Massaad, Charbel
; APPLICANT: Berenbaum, Francis
; APPLICANT: Olivier, Jean-Luc
; APPLICANT: Salvat, Colette
; APPLICANT: Bereziat, Gilbert
; TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising them
; FILE REFERENCE: ST00010
; CURRENT APPLICATION NUMBER: US/09/808,388
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: FR/00/03262
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/196,959
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: PP68 element
US-09-808-388-2

Query Match 100.0%; Score 20; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAACTAGGTCAAAGGTCA 20
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us-09-808-388-1.sept04.rnpb

Mon Sep 13 07:48:08 2004

Db 1 CAAACTAGGTCAAAGGTCA 20

RESULT 11

US-09-808-388-3
; Sequence 3, Application US/09808388
; Patent No. US20020081719A1
; GENERAL INFORMATION:
; APPLICANT: Massaad, Charbel
; APPLICANT: Berenbaum, Francis
; APPLICANT: Olivier, Jean-Luc
; APPLICANT: Salvat, Colette
; APPLICANT: Bereziat, Gilbert
; TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising them
; FILE REFERENCE: ST00010
; CURRENT APPLICATION NUMBER: US/09/808,388
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: FR/00/03262
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/196,959
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PPPE element
US-09-808-388-3

Query Match 100.0%; Score 20; DB 9; Length 41;
Best Local Similarity 100.0%; Pred. No. 3.3; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1 CAAACTAGGTCAAAGGTCA 20
Db 1 CAAACTAGGTCAAAGGTCA 20

RESULT 12

US-09-808-388-4
; Sequence 4, Application US/09808388
; Patent No. US20020081719A1
; GENERAL INFORMATION:
; APPLICANT: Massaad, Charbel
; APPLICANT: Berenbaum, Francis
; APPLICANT: Olivier, Jean-Luc
; APPLICANT: Salvat, Colette
; APPLICANT: Bereziat, Gilbert
; TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising them
; FILE REFERENCE: ST00010
; CURRENT APPLICATION NUMBER: US/09/808,388
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: FR/00/03262
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/196,959
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PPPE element
US-09-808-388-4

Query Match 100.0%; Score 20; DB 9; Length 52;
Best Local Similarity 100.0%; Pred. No. 3.4; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1 CAAACTAGGTCAAAGGTCA 20
Db 1 CAAACTAGGTCAAAGGTCA 20

RESULT 13

US-09-877-705A-142/c
; Sequence 142, Application US/09877705A
; Publication No. US20030008283A1
; GENERAL INFORMATION:
; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD FOR SCREENING FOR DRUG CANDIDATES FOR MODULATING TRANSCRIPTION FACTOR-PROTEIN INTERACTIONS
; FILE REFERENCE: 26757-704
; CURRENT APPLICATION NUMBER: US/09/877,705A
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 142
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hybridization probe MP68
US-09-877-705A-142

Query Match 100.0%; Score 20; DB 10; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.5; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1 CAAACTAGGTCAAAGGTCA 20
Db 60 CAAACTAGGTCAAAGGTCA 41

RESULT 14

US-09-877-738A-142/c
; Sequence 142, Application US/09877738A
; Publication No. US20030022173A1
; GENERAL INFORMATION:
; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED TRANSCRIPTION FACTORS
; FILE REFERENCE: 26757-701
; CURRENT APPLICATION NUMBER: US/09/877,738A
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 142
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hybridization probe MP68
US-09-877-738A-142

Query Match 100.0%; Score 20; DB 10; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.5; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1 CAAACTAGGTCAAAGGTCA 20
Db 60 CAAACTAGGTCAAAGGTCA 41

RESULT 15

US-09-947-274-142/c
; Sequence 142, Application US/09947274
; Publication No. US20030017499A1
; GENERAL INFORMATION:
; APPLICANT: Li, Xiangqiang
; TITLE OF INVENTION: METHOD FOR DETECTING TRANSCRIPTION FACTOR-PROTEIN INTERACTIONS


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; FILE REFERENCE: 26757-705
; CURRENT APPLICATION NUMBER: US/09/947,274
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 09/877,738
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/877,243
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/877,403
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/877,705
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 142
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hybridization probe MP68
US-09-947-274-142

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Query Match      100.0%; Score 20; DB 13; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CAAAACTAGGTCAAAGGTCA 20
        |||||
Db      60 CAAAACTAGGTCAAAGGTCA 41

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Search completed: September 11, 2004, 14:11:08
Job time : 20.3993 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 08:16:17 ; Search time 3.14488 Seconds
(without alignments)
3529.238 Million cell updates/sec

Title: US-09-808-388-1

Perfect score: 20

Sequence: 1 caaaactagggtcaaaaggtca 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

- 1: /cgn2_6/prodata/2/ina/5A COMB.seq.*
- 2: /cgn2_6/prodata/2/ina/5B COMB.seq.*
- 3: /cgn2_6/prodata/2/ina/6A COMB.seq.*
- 4: /cgn2_6/prodata/2/ina/6B COMB.seq.*
- 5: /cgn2_6/prodata/2/ina/PCTUS COMB.seq.*
- 6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15.8	79.0	421	4	US-09-621-976-12838
C 2	15.4	77.0	587	3	US-09-053-702-3
C 3	15.2	76.0	3441	2	US-08-742-753-1
C 4	15.2	76.0	13865	3	US-09-009-217-11
C 5	15.2	76.0	13865	3	US-09-009-656-11
C 6	15.2	76.0	15894	1	US-08-348-891A-1
C 7	15.2	76.0	15894	1	US-08-905-817-1
C 8	15.2	76.0	580073	4	US-08-545-528D-1
C 9	15.2	75.0	2661	1	US-08-351-413-1
C 10	15.2	75.0	2661	2	US-09-025-583-1
C 11	15.2	75.0	4808	1	US-08-351-413-17
C 12	15.2	75.0	4808	2	US-09-025-583-17
C 13	14.8	74.0	328	4	US-09-621-976-9939
C 14	14.8	74.0	1140	4	US-09-328-352-1678
C 15	14.8	74.0	11303	4	US-08-961-527-115
C 16	14.8	74.0	14485	4	US-09-876-216-3
C 17	14.8	74.0	16595	4	US-09-146-053-7
C 18	14.8	74.0	118067	4	US-09-497-855A-32
C 19	14.4	72.0	480	4	US-09-134-000C-778
C 20	14.4	72.0	2372	4	US-09-620-312D-763
C 21	14.4	72.0	3127	4	US-09-620-312D-613
C 22	14.4	72.0	56804	4	US-09-740-041-3
C 23	14.4	72.0	161652	4	US-09-497-855A-40
C 24	14.4	72.0	1830121	4	US-09-557-884-1
C 25	14.4	72.0	1830121	4	US-09-643-990A-1
C 26	14.2	71.0	468	4	US-09-621-976-784
C 27	14.2	71.0	865	3	US-09-328-111-128

Sequence 3, Appli
Sequence 1308, Ap
Sequence 5681, Ap
Sequence 16, Appl
Sequence 3628, Ap
Sequence 1501, Ap
Sequence 37, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 990, App
Sequence 2, Appli
Sequence 2, Appli
Sequence 1022, Ap
Sequence 7, Appli
Sequence 48, Appl
Sequence 48, Appl
Sequence 48, Appl

28 14.2 71.0 1026 4 US-09-394-110A-3
29 14.2 71.0 1236 4 US-09-543-681A-1308
C 30 14.2 71.0 1284 4 US-09-489-039A-5681
C 31 14.2 71.0 1288 4 US-09-724-864-16
C 32 14.2 71.0 1288 4 US-09-328-352-3628
C 33 14.2 71.0 1704 4 US-09-543-681A-1501
C 34 14.2 71.0 1846 4 US-09-336-536-37
C 35 14.2 71.0 2103 3 US-08-931-952-1
C 36 14.2 71.0 2103 3 US-08-272-247-1
C 37 14.2 71.0 2103 5 PCT-US95-08560-1
C 38 14.2 71.0 2849 4 US-09-221-017B-990
C 39 14.2 71.0 2964 2 US-08-846-790A-2
C 40 14.2 71.0 2964 3 US-08-935-333-2
C 41 14.2 71.0 3083 4 US-09-976-594-1022
C 42 14.2 71.0 3095 4 US-09-293-549-7
C 43 14.2 71.0 5521 3 US-08-975-762-48
C 44 14.2 71.0 5521 3 US-09-295-028-48
C 45 14.2 71.0 5521 4 US-09-106-582-48

ALIGNMENTS

RESULT 1
US-09-621-976-12838/c
; Sequence 12838, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 12838
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-12838

Query Match 79.0%; Score 15.8; DB 4; Length 421;
Best Local Similarity 89.5%; Pred. No. 32;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAAAAGTGGTCAAGGTCA 20
Db 162 AAAAAGTGGTCAAGGTCA 144

RESULT 2
US-09-053-702-3/c
; Sequence 3, Application US/09053702
; Patent No. 6229069
; GENERAL INFORMATION:
; APPLICANT: YAMADA, Shigehiro
; TITLE OF INVENTION: METHOD FOR CONTROLLING WATER CONTENT OF PLANT
; FILE REFERENCE: 230-122P
; CURRENT APPLICATION NUMBER: US/09/053,702
; CURRENT FILING DATE: 1998-04-02
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 587
; TYPE: DNA
; ORGANISM: Nicotiana tabacum
US-09-053-702-3

Query Match 77.0%; Score 15.4; DB 3; Length 587;
Best Local Similarity 94.1%; Pred. No. 55;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


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/ FILING DATE: Concurrently Herewith
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/042,427
/ FILING DATE: 27-MAR-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/036,205
/ FILING DATE: 27-JAN-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/035,920
/ FILING DATE: 22-JAN-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hibler, David W.
/ REGISTRATION NUMBER: 41,071
/ REFERENCE/DOCKET NUMBER: UTSD:537
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 512/418-3000
/ TELEFAX: 512/474-7577
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 13865 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-09-009-656-11

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Query Match          76.0%; Score 15.2; DB 3; Length 13865;
Best Local Similarity 85.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY      1 CAAACTAGGTCAAGTGCA 20
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Db      13773 CAAATTAGGTAAAGGACA 13792

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RESULT 6
US-08-348-891A-1/c
; Sequence 1, Application US/08348891A
; Patent No. 5654136
; GENERAL INFORMATION:
; APPLICANT: SASAKI, Keiko
; APPLICANT: MORI, Takayuki
; APPLICANT: MAKINO, Satoshi
; TITLE OF INVENTION: ATTENUATED MEASLES VIRUS VACCINE,
; TITLE OF INVENTION: CONTAINING SPECIFIC NUCLEOTIDE SEQUENCE AND A METHOD FOR
; TITLE OF INVENTION: ITS ABSOLUTE IDENTIFICATION
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/348,891A
; FILING DATE: 25-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,400
; FILING DATE: 10-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-293625
; FILING DATE: 14-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: KB-7501

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/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 703-521-2297
/ TELEFAX: 703-685-0573
/ TELEX: 248425 EMBON
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15894 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 108..1682
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1807..3327
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 3438..4442
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 5458..7107
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 7271..9121
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 9234..15782
/ US-08-348-891A-1

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Query Match          76.0%; Score 15.2; DB 1; Length 15894;
Best Local Similarity 85.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY      1 CAAACTAGGTCAAGTGCA 20
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Db      9920 CAAACCAGTCAAGTGCA 9901

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RESULT 7
US-08-905-817-1/c
; Sequence 1, Application US/08905817
; Patent No. 5824777
; GENERAL INFORMATION:
; APPLICANT: SASAKI, Keiko
; APPLICANT: MORI, Takayuki
; APPLICANT: MAKINO, Satoshi
; TITLE OF INVENTION: ATTENUATED MEASLES VIRUS VACCINE,
; TITLE OF INVENTION: CONTAINING SPECIFIC NUCLEOTIDE SEQUENCE AND A METHOD FOR
; TITLE OF INVENTION: ITS ABSOLUTE IDENTIFICATION
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,817
; FILING DATE: 04-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,891
; FILING DATE: 25-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,400

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us-09-808-388-1.sept04.rni

Mon Sep 13 07:48:08 2004

Best Local Similarity 85.0%; Pred. No. 2.2e+02; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 3;

QY 1 CAAACTAGTCAAGGTCA 20
Db 21486 CAAACAAGATCAAGATCA 21467

RESULT 9

US-08-351-413-1
; Sequence 1, Application US/08351413
; Patent No. 5750867
; GENERAL INFORMATION:
; APPLICANT: Williams, Mark
; APPLICANT: Leemans, Jan
; TITLE OF INVENTION: Maintenance of male-sterile plants
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 2046
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/351,413
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/899,072
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/970,849
; FILING DATE: 03-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 2121-102PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2661 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Zea mays
; STRAIN: inbred line W-22
; PUBLICATION INFORMATION:
; AUTHORS: Hamilton et al.,
; JOURNAL: Sex Plant Reprod.
; VOLUME: 2
; PAGES: 208-
; DATE: 1989
; US-08-351-413-1

Query Match 75.0%; Score 15; DB 1; Length 2661;
Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 1 CAAACTAGTCAAGGTCA 15
Db 21486 CAAACAAGATCAAGATCA 21467

FILING DATE: 10-MAR-1992
PRIOR APPLICATION DATA: JP 3-293625
APPLICATION NUMBER: 14-OCT-1991
FILING DATE: 14-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: KP-7501A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-521-2297
TELEFAX: 703-685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 108..1682
FEATURE:
NAME/KEY: CDS
LOCATION: 1807..3327
FEATURE:
NAME/KEY: CDS
LOCATION: 3438..4442
FEATURE:
NAME/KEY: CDS
LOCATION: 5458..7107
FEATURE:
NAME/KEY: CDS
LOCATION: 7271..9121
FEATURE:
NAME/KEY: CDS
LOCATION: 9234..15782

Query Match 76.0%; Score 15.2; DB 1; Length 15894;
Best Local Similarity 85.0%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 3;

QY 1 CAAACTAGTCAAGGTCA 20
Db 9920 CAAACAGTCAAGTCA 9901

RESULT 8

US-08-545-528D-1/c
; Sequence 1, Application US/08545528D
; Patent No. 6537773
; GENERAL INFORMATION:
; APPLICANT: Fraser et al.
; TITLE OF INVENTION: Nucleotide sequence of the Mycoplasma genitalium Genome, Fragment
; PATENT NO. 6537773
; TITLE OF INVENTION: Thereof, and Uses Thereof
; FILE REFERENCE: PBI93P1
; CURRENT APPLICATION NUMBER: US/08/545,528D
; CURRENT FILING DATE: 1995-10-19
; PRIOR APPLICATION NUMBER: US 08/488,018
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/473,545
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 3.1
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 580073
; TYPE: DNA
; ORGANISM: Mycoplasma genitalium
; US-08-545-528D-1

Query Match 76.0%; Score 15.2; DB 4; Length 580073;

Db 1180 CAAACTAGGTCAA 1194

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RESULT 10
US-09-025-583-1
; Sequence 1, Application US/09025583
; Patent No. 5977433
; GENERAL INFORMATION:
; APPLICANT: Williams, Mark
; APPLICANT: Leemans, Jan
; TITLE OF INVENTION: Maintenance of male-sterile plants
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 2046
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,583
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/351,413
; FILING DATE:
; APPLICATION NUMBER: US 07/899,072
; FILING DATE: 12-JUN-1992
; APPLICATION NUMBER: US 07/970,849
; FILING DATE: 03-NOV-1992
; APPLICATION DATA:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 2121-102PCT
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2661 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Zea mays
; STRAIN: inbred line W-22
; PUBLICATION INFORMATION:
; AUTHORS: Hamilton et al.,
; JOURNAL: Sex Plant Reprod.
; VOLUME: 2
; PAGES: 208-
; DATE: 1989
US-09-025-583-1
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Query Match 75.0%; Score 15; DB 2; Length 2661;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAACTAGGTCAA 15

Db 1180 CAAACTAGGTCAA 1194

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RESULT 11
US-08-351-413-17/c
; Sequence 17, Application US/08351413
; Patent No. 5750867
; GENERAL INFORMATION:
; APPLICANT: Williams, Mark
; APPLICANT: Leemans, Jan
; TITLE OF INVENTION: Maintenance of male-sterile plants
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 2046
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/351,413
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/899,072
; FILING DATE: 12-JUN-1992
; APPLICATION NUMBER: US 07/970,849
; FILING DATE: 03-NOV-1992
; APPLICATION DATA:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 2121-102PCT
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4808 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: EcoRI-HindIII fragment of plasmid pTS218
; FEATURE:
; NAME/KEY: -
; LOCATION: complement (18..401)
; OTHER INFORMATION: /label= 3'nos
; OTHER INFORMATION: /note= "3' regulatory sequence containing the
; OTHER INFORMATION: polyadenylation site derived from Agrobacterium
; OTHER INFORMATION: T-DNA nopaline synthase gene"
; FEATURE:
; NAME/KEY: -
; LOCATION: complement (402..737)
; OTHER INFORMATION: /label= barnase
; OTHER INFORMATION: /note= "coding region of the barnase gene of
; OTHER INFORMATION: Bacillus amyloliquefaciens"
; FEATURE:
; NAME/KEY: -
; LOCATION: complement (738..1944)
; OTHER INFORMATION: /label= PZM13
; OTHER INFORMATION: /note= "promoter region of the Zml3 gene of Zea
; OTHER INFORMATION: mays"
; FEATURE:
; NAME/KEY: -
; LOCATION: complement (1945..2281)
; OTHER INFORMATION: /label= 3'nos
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us-09-808-388-1.sept04.rni

Mon Sep 13 07:48:08 2004

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FEATURE:
NAME/KEY: - complement (2282..2554)
LOCATION: /label= barstar
OTHER INFORMATION: /note= "coding region of the barstar gene of
OTHER INFORMATION: Bacillus amyloliquefaciens"
FEATURE:
NAME/KEY: - complement (2555..3099)
LOCATION: /label= PTA29
OTHER INFORMATION: /note= "promoter region of the TA29 gene of
OTHER INFORMATION: Nicotiana tabacum"
FEATURE:
NAME/KEY: - 3100..3932
LOCATION: /label= 3583
OTHER INFORMATION: /note= "35S3" promoter sequence derived from
OTHER INFORMATION: cauliflower mosaic virus isolate Cabbb-J1"
FEATURE:
NAME/KEY: - 3933..4484
LOCATION: /label= bar
OTHER INFORMATION: /note= "coding region of the phosphinothricin
OTHER INFORMATION: acetyltransferase gene"
FEATURE:
NAME/KEY: - 4485..4763
LOCATION: /label= 3'nos
OTHER INFORMATION:
FEATURE:
NAME/KEY: - 2333..2356
LOCATION: /label= BXOL2
OTHER INFORMATION: /note= "region corresponding to oligonucleotide
OTHER INFORMATION: BXOL2"
FEATURE:
NAME/KEY: - complement (2538..2586)
LOCATION: /label= TA29SBXOL2
OTHER INFORMATION: /note= "region complementary to oligonucleotide
OTHER INFORMATION: TA29SBXOL2"
FEATURE:
NAME/KEY: - complement (2800..2823)
LOCATION: /label= PTA29OL5
OTHER INFORMATION: /note= "region complementary to part of
OTHER INFORMATION: oligonucleotide PTA29OL5"
US-08-351-413-17
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CAAAACTAGGTCAAA 15
Db 984 CAAAACTAGGTCAAA 970
RESULT 12
US-09-025-583-17/c
Sequence 17, Application US/09025583
Patent No. 5977433
GENERAL INFORMATION:
APPLICANT: Williams, Mark
APPLICANT: Leemans, Jan
TITLE OF INVENTION: Maintenance of male-sterile plants
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 2046
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,583
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/351,413
FILING DATE:
APPLICATION NUMBER: US 07/899,072
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/970,849
FILING DATE: 03-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 2121-102PCT
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 4808 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: EcorI-HindIII fragment of plasmid pTS218
FEATURE:
NAME/KEY: -
LOCATION: complement (18..401)
OTHER INFORMATION: /label= 3'nos
OTHER INFORMATION: /note= "3' regulatory sequence containing the
OTHER INFORMATION: polyadenylation site derived from Agrobacterium
OTHER INFORMATION: T-DNA nopaline synthase gene"
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NAME/KEY: -
LOCATION: complement (402..737)
OTHER INFORMATION: /label= barnase
OTHER INFORMATION: /note= "coding region of the barnase gene of
OTHER INFORMATION: Bacillus amyloliquefaciens"
FEATURE:
NAME/KEY: -
LOCATION: complement (738..1944)
OTHER INFORMATION: /label= P2M13
OTHER INFORMATION: /note= "promoter region of the Zml3 gene of Zea
OTHER INFORMATION: mays"
FEATURE:
NAME/KEY: -
LOCATION: complement (1945..2281)
OTHER INFORMATION: /label= 3'nos
FEATURE:
NAME/KEY: -
LOCATION: complement (2282..2554)
OTHER INFORMATION: /label= barstar
OTHER INFORMATION: /note= "coding region of the barstar gene of
OTHER INFORMATION: Bacillus amyloliquefaciens"
FEATURE:
NAME/KEY: -
LOCATION: complement (2555..3099)
OTHER INFORMATION: /label= PTA29
OTHER INFORMATION: /note= "promoter region of the TA29 gene of
OTHER INFORMATION: Nicotiana tabacum"
FEATURE:
NAME/KEY: -

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; LOCATION: 3100...3932
; OTHER INFORMATION: /label= 3583
; /note= "35S3" promoter sequence derived from
; OTHER INFORMATION: cauliflower mosaic virus isolate CabbB-J1"
; FEATURE:
; NAME/KEY: -
; LOCATION: 3933...4484
; OTHER INFORMATION: /label= bar
; /note= "coding region of the phosphinothricin
; OTHER INFORMATION: acetyltransferase gene"
; FEATURE:
; NAME/KEY: -
; LOCATION: 4485...4763
; OTHER INFORMATION: /label= 3'nos
; FEATURE:
; NAME/KEY: -
; LOCATION: 2333...2356
; OTHER INFORMATION: /label= BXOL2
; /note= "region corresponding to oligonucleotide
; OTHER INFORMATION: BXOL2"
; FEATURE:
; NAME/KEY: -
; LOCATION: complement (2538..2586)
; /label= TA29SBXOL2
; OTHER INFORMATION: /note= "region complementary to oligonucleotide
; OTHER INFORMATION: TA29SBXOL2"
; FEATURE:
; NAME/KEY: -
; LOCATION: complement (2800..2823)
; /label= PTA29OL5
; OTHER INFORMATION: /note= "region complementary to part of
; OTHER INFORMATION: oligonucleotide PTA29OL5"
US-09-025-583-17

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Query Match          75.0%; Score 15; DB 2; Length 4808;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CAAACTAGGTCAA 15
    |||||
Db 984 CAAACTAGGTCAA 970

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RESULT 13
US-09-621-976-9939
; Sequence 9939, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 9939
; LENGTH: 328
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-9939

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Query Match          74.0%; Score 14.8; DB 4; Length 328;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 3 AAACCTAGGTCAAAGTCA 20
    |||||
Db 31 AAACCAAGGTCAAAGGTGA 48

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RESULT 14

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US-09-328-352-1678/c
; Sequence 1678, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: GTC99-03PA
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 1678
; LENGTH: 1140
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-1678

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Query Match          74.0%; Score 14.8; DB 4; Length 1140;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 2 AAACCTAGGTCAAAGTTC 19
    |||||
Db 986 AAAGCTTGGTCAAAGTTC 969

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RESULT 15

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US-08-961-527-115/c
; Sequence 115, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11303 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-115

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Query Match          74.0%; Score 14.8; DB 4; Length 11303;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 CAAACTAGGTCAAAGGT 18

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us-09-808-388-1.sept04.rni

Mon Sep 13 07:48:08 2004

Db 7784 CAAAACAGGTCRAGGT 7767
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Search completed: September 11, 2004, 09:33:09
Job time : 7.14488 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 06:05:16 ; Search time 2754 Seconds
(without alignments)
1897.560 Million cell updates/sec

Title: US-09-808-388-5_COPY_1_175
Perfect score: 175
Sequence: 1 cgcggcaaaactgctgaaa.....tccccagcctgtgcttcac 175

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST.*

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estmu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_htc.*

9: gb_est1.*

10: gb_est2.*

11: gb_htc.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_mam.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

26: em_gss_phg.*

27: em_gss_vrl.*

28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34.8	19.9	1201	9	AL525279
2	34.4	19.7	357	14	N75549
3	33.8	19.3	368	9	AA565892
4	33.6	19.2	600	12	BG803927

C	5	33.4	19.1	507	10	BE754755
C	6	33	18.9	941	12	BM451198
C	7	32.4	18.5	474	14	T71683
C	8	32.2	18.4	723	29	CC904751
C	9	32	18.3	370	9	AI453680
C	10	32	18.3	392	9	AA405428
C	11	32	18.3	425	10	AA467514
C	12	32	18.3	449	10	BE300996
C	13	32	18.3	454	14	CB819052
C	14	32	18.3	553	10	BE237161
C	15	31.8	18.2	995	9	AL570803
C	16	31.6	18.1	422	14	CB105190
C	17	31.6	18.1	467	9	AI955727
C	18	31.6	18.1	724	12	BI822441
C	19	31.6	18.1	784	12	BI088973
C	20	31.6	18.1	1087	12	BM458295
C	21	31.4	17.9	350	10	BF394189
C	22	31.4	17.9	430	13	BY186932
C	23	31.4	17.9	810	29	EX176093
C	24	31.4	17.9	1059	28	CC271850
C	25	31.4	17.9	1141	12	BG122709
C	26	31.2	17.8	272	10	BF888447
C	27	31.2	17.8	348	9	AA701617
C	28	31.2	17.8	409	28	BZ345401
C	29	31.2	17.8	676	14	CA249326
C	30	31.2	17.8	693	14	CA172179
C	31	31.2	17.8	874	13	BU201102
C	32	31.2	17.8	910	14	CA280524
C	33	31	17.7	643	12	BG415781
C	34	31	17.7	907	29	CNS05515
C	35	31	17.7	1028	14	CB563160
C	36	31	17.7	1083	13	BQ058613
C	37	30.8	17.6	366	13	BU984495
C	38	30.8	17.6	413	12	BG829037
C	39	30.8	17.6	523	10	BG078896
C	40	30.8	17.6	629	14	CB875655
C	41	30.8	17.6	812	13	BQ229858
C	42	30.8	17.6	898	13	BU187886
C	43	30.8	17.6	925	13	BQ714058
C	44	30.8	17.6	1059	12	BM470242
C	45	30.8	17.6	1088	12	BM544574

ALIGNMENTS

RESULT 1

AL525279

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AL525279 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
cDNA clone CS0DC011YC03 3-PRIME, mRNA sequence.
1201 bp mRNA linear EST 22-MAY-2003

AL525279.2 GI:31043534

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)

Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 13, 2001 this sequence version replaced gi:12788772.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 9221.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DC011AB02NP1&cluster=9221.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :


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QY 3 CGGCAAACTGCTGAATGTGTTTGGCATCTACTGACAGTAAAGCTTCCCAATC 62
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
229 CGGCAAAATAACGAGCATGTGTGTGAACATCCCCCAGTGGCGGTAGGAATCCCCCATG 288
QY 63 CTCAACTCTGCTCCGACGCTGATGAGGGAAGGAAGGGA 103
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
289 GTGACCTGTGACCTGTCTCCCTGAGACAGGGGAGGCCAGGCA 329

RESULT 4
BG803927 600 bp mRNA linear EST 20-DEC-2001
LOCUS 0243-51 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,
DEFINITION mRNA sequence.
ACCESSION BG803927
VERSION BG803927.1 GI:17950840
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 600)
Mu.X., Zhao, S., Pershad, R., Hsieh, T.-F., Scarpa, A., Wang, S.W.,
White, R.A., Beremand, P.D., Thomas, T.L., Gan, L. and Klein, W.H.
Gene expression in the developing mouse retina by EST sequencing
and microarray analysis
Nucleic Acids Res. 29 (24), 4983-4993 (2001)
21671825
11812828
Contact: Klein WH
Department of Biochemistry and Molecular Biology
University of Texas M.D. Anderson Cancer Center
Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
Tel: 713 792 3646
Fax: 713 790 0329.
FEATURES
Location/Qualifiers
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1..600
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/tissue_type="neural retina"
/dev_stage="embryonic day 14.5 post-fertilization"
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Query Match 19.2%; Score 33.6; DB 12; Length 600;
Best Local Similarity 56.2%; Pred. No. 12;
Matches 63; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 63 CTCAACTCTGCTCCGACGCTGATGAGGGAAGGAAGGGA 122
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QY 123 ACCAATCTGAGTCCACCACTGACACGCGCCATCCCGCCTTGTCCTCA 174
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
161 ACCAGACTGAGGTCTTCTGCGGCCCGCCCGCCCGCCAGAGCCTCTCTCA 212

RESULT 5
BE754755/c 507 bp mRNA linear EST 25-APR-2001
LOCUS 208358 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE754755
VERSION BE754755.1 GI:10168747
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 507)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,

QY 3 CGGCAAACTGCTGAATGTGTTTGGCATCTACTGACAGTAAAGCTTCCCAATC 62
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
229 CGGCAAAATAACGAGCATGTGTGTGAACATCCCCCAGTGGCGGTAGGAATCCCCCATG 288
QY 63 CTCAACTCTGCTCCGACGCTGATGAGGGAAGGAAGGGA 103
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
289 GTGACCTGTGACCTGTCTCCCTGAGACAGGGGAGGCCAGGCA 329

RESULT 4
BG803927 600 bp mRNA linear EST 20-DEC-2001
LOCUS 0243-51 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,
DEFINITION mRNA sequence.
ACCESSION BG803927
VERSION BG803927.1 GI:17950840
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 600)
Mu.X., Zhao, S., Pershad, R., Hsieh, T.-F., Scarpa, A., Wang, S.W.,
White, R.A., Beremand, P.D., Thomas, T.L., Gan, L. and Klein, W.H.
Gene expression in the developing mouse retina by EST sequencing
and microarray analysis
Nucleic Acids Res. 29 (24), 4983-4993 (2001)
21671825
11812828
Contact: Klein WH
Department of Biochemistry and Molecular Biology
University of Texas M.D. Anderson Cancer Center
Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
Tel: 713 792 3646
Fax: 713 790 0329.
FEATURES
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/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/tissue_type="neural retina"
/dev_stage="embryonic day 14.5 post-fertilization"
/clone_lib="Mouse E14.5 retina lambda ZAP II Library"

ORIGIN
Query Match 19.2%; Score 33.6; DB 12; Length 600;
Best Local Similarity 56.2%; Pred. No. 12;
Matches 63; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 63 CTCAACTCTGCTCCGACGCTGATGAGGGAAGGAAGGGA 122
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
101 CTCAGCTCTGCTCGTGGAGGAGCGACTGGACAGAGAGTCGTGGGGTGGCAGTG 160
QY 123 ACCAATCTGAGTCCACCACTGACACGCGCCATCCCGCCTTGTCCTCA 174
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
161 ACCAGACTGAGGTCTTCTGCGGCCCGCCCGCCCGCCAGAGCCTCTCTCA 212

RESULT 5
BE754755/c 507 bp mRNA linear EST 25-APR-2001
LOCUS 208358 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE754755
VERSION BE754755.1 GI:10168747
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 507)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,

```

```

Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
Chitko-McKown, C.G., Perlea, G., Holt, I., Karamycheva, S., Liang, F.,
Quackenbush, J. and Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
11282978
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.960904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACACGTATGACCAT
BACKWARD: GTTTCGCCAGTCACGAG
Plate: 55 row: O column: 10
Seq primer: ATTAGGTGACACTATAG.
Location/Qualifiers
1..507
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 2BOV"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from testis, thymus,
semitendinosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."

ORIGIN
Query Match 19.1%; Score 33.4; DB 10; Length 507;
Best Local Similarity 53.4%; Pred. No. 12;
Matches 70; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 43 ACAGTAAAGTTTCCCAATCTCAACTCTCTCTGCCAGCTGATGAGGGAAGGAAGGG 102
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
449 ACATGAAGTTTCCATCTCTATCGGCTCCAGCACTCTGTATCGACCGCCAC 390
QY 103 ATTACCTAGGGGTATGGGACCAATCTGAGTCCACCAACTGACCGCCCATCCCCAG 162
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
389 ATGAATCGGTATTGCCCTACCAGTCTTGCCGTCACAGTGGACCATCAGCTTTCCCG 330
QY 163 CCTGTGCCTC 173
Db ||||| |||||
329 ACCTGAGCCTC 319

RESULT 6
BM451198/c 941 bp mRNA linear EST 05-FEB-2002
LOCUS AGENCOURT_6392622 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5495177
DEFINITION 5', mRNA sequence.
ACCESSION BM451198
VERSION BM451198.1 GI:18500238
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 941)
NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC

```

High quality sequence stop: 338.

FEATURES
source
Location/Qualifiers
1. 474

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM12121 row: k column: 18
High quality sequence stop: 632.

FEATURES
source
Location/Qualifiers
1. 941

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5495177"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 67"
/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.75 kb. Library constructed by Life
Technologies."

ORIGIN
Query Match 18.9%; Score 33; DB 12; Length 941;
Best Local Similarity 54.5%; Pred. No. 23;
Matches 60; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 54 TTCCCAATCCTCAACTCTCTCTCCAGCTGATGAGGGAAGGAGGATACCTAGG 113
DB 716 TTCAAGATCAGGTCGGCTCGTCTGATGTCGAGGATGCTGGGAGCATCCCTCC 657
QY 114 GTATGGCGACCAATCCTGAGTCCCAACTGACCAAGCCATCCCGCCAGC 163
DB 656 ATCTGGGGANNCTTCCCAACCCACCCCTGTCACCGCCAGCCACAGC 607

RESULT 7
T71683
LOCUS
DEFINITION
yc62h05.s1 StrataGene liver (#937224) Homo sapiens cDNA clone
IMAGE:85305 3' similar to gb:J03048 HEMOPXIN PRECURSOR (HUMAN);
mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
T71683.1 GI:686204
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
Hillier L., Lennon G., Becker M., Bonaldo M.F., Chiapelli B.,
Chisoe S., Dietrich N., DuBuque T., Favello A., Gish W.,
Hawkins M., Hultman M., Kucaba T., Lacy M., Le M., Le N.,
Mardis E., Moore B., Morris M., Parsons J., Prange C., Rifkin L.,
Roellig T., Schellenberg K., Soares M.B., Tan F., Thierry-Mieg J.,
Trevisan E., Underwood K., Wohlmann P., Watson R., Wilson R.,
and Marra M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
Insert Size: 511
High quality sequence stops: 338 Source: IMAGE Consortium, LLNL This
clone is available royalty-free through LLNL; contact the IMAGE
Consortium (info@image.llnl.gov) for further information.
Insert Length: 511 Std Error: 0.00
Seq primer: -21m13

FEATURES
source
Location/Qualifiers
1. 474

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:502362"
/db_xref="taxon:9606"
/clone="IMAGE:85305"
/sex="male"
/dev_stage="49 years old"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene liver (#937224)"
/note="Organ: liver; Vector: pBluescript SK; Site 1:
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. Hepatectomy from normal male caucasian. Average
insert size: 1.1 kb; Uni-ZAP XR Vector; ~5' adaptor
sequence: 5' GAATTCGGCAGAG 3' ~3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTT 3"

ORIGIN

Query Match 18.5%; Score 32.4; DB 14; Length 474;
Best Local Similarity 53.7%; Pred. No. 25;
Matches 66; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
QY 31 CATCAGCTACTGACACGTAAGGTTTCCCAATCCTCAACTCTGCTCCGCGCTGATGAGG 90
DB 296 CATGAGTTAGGCGCAAGGACTTTTCCATACACAGGCTCGCTTACTCTTTCATGGG 355
QY 91 GGAAGGAAGGATTTACCTAGGGTATGGGAGCAATCCTGAGTCCCAACTGACCAAC 150
DB 356 CCAAGGAAGCTCTCTCCACGTGGCTTGGGCTCTGACTTCAAGTCCAGCCACCAAGCC 415

QY 151 GCC 153
DB 416 GCC 418

RESULT 8
CC904751
LOCUS
DEFINITION

t015m08ba.r1 TAMBT Bos taurus genomic clone t015m08ba, genomic
survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
CC904751.1 GI:33523684
GSS.
Bos taurus (cow)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Lin, S., Najjar, F. Z., Adelson, D., Gill, C. A. and Roe, B. A.
1. (bases 1 to 723)
Bovine BAC End Sequences from Library TAMBT
Unpublished (2003)
Contact: Bruce A. Roe
Advanced Center for Genome Technology
University of Oklahoma Department of Chemistry and Biochemistry
620 Parrington Oval, Room 208, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Class: BAC ends
High quality sequence stop: 367.

FEATURES
source
Location/Qualifiers
1. 723

/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="Angus Bull T A M U Shoshone Y6 11519666"
/db_xref="taxon:9913"
/clone="t015m08ba"
/sex="Male"
/cell_type="Blood"
/clone_lib="TAMBT"

Mon Sep 13 07:48:10 2004

National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE
JOURNAL
COMMENT

RESULT 11
AW467514 425 bp mRNA linear EST 24-FEB-2000
LOCUS
DEFINITION
he19g02.x1 NCI CGAP CML1 Homo sapiens cDNA clone IMAGE:2919506 3',
similar to contains element MER31 repetitive element ;, mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AW467514 GI:7037620
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 425)
NCI CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov

Tissue Procurement: Elisabeth Paletta, Jonathan D. Licht, M.D.,
Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christina Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrrp/image/image.html
Seq primer: -400P from Gibco
High quality sequence stop: 421.

FEATURES
Source
1. .425
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2919506"
/tissue type="myeloid cells, 18 pooled CML cases, BCR/ABL
rearrangement positive, includes both chronic phase and
myeloid blast crisis"
/lab host="DH10B"
/clone_lib="NCI CGAP CML1"
/notes="Organ: whole blood; Vector: pCMV-Sport6; Site 1:
Sali; Site 2: NotI; Cloned unidirectionally. Primer:
Oligo dt. Library constructed by Life Technologies."

ORIGIN
Query Match 18.3%; Score 32; DB 10; Length 425;
Best Local Similarity 55.4%; Pred. No. 31; Indels 0; Gaps 0;
Matches 62; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 3 CGGCAAACTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAATC 62
Db 233 CGCCAAATACACGATGTTGTTAAATCCCCCAGTGGGGCTAGAAATCCCCATG 292
QY 63 CTCACCTCTGTCGCGCAGTGTAGCGGAGGAAAGGATACCTAGGGG 114
Db 293 GTGACCTGTGACCTGCTCCCTGAGACAGGGAGGCCAGGCATGCACGGTGG 344

RESULT 12
BE300996 449 bp mRNA linear EST 14-JUL-2000
LOCUS
DEFINITION
ba2b05.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2906865 3',
mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BE300996 GI:9184744
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 449)
NIH-MGC <http://mgc.nci.nih.gov/>.

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov

Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -400P from Gibco
High quality sequence stop: 437.

FEATURES
Location/Qualifiers
1. .449
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2906865"
/tissue type="choriocarcinoma"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_21"
/note="Organ: placenta; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected 500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN
Query Match 18.3%; Score 32; DB 10; Length 449;
Best Local Similarity 55.4%; Pred. No. 32;
Matches 62; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 3 CGGCAAACTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAATC 62
Db 233 CGCCAAATACACGATGTTGTTAAATCCCCCAGTGGGGCTAGAAATCCCCATG 292
QY 63 CTCACCTCTGTCGCGCAGTGTAGCGGAGGAAAGGATACCTAGGGG 114
Db 293 GTGACCTGTGACCTGCTCCCTGAGACAGGGAGGCCAGGCATGCATGTTGG 344

RESULT 13
CB819052 454 bp mRNA linear EST 16-MAY-2003
LOCUS
DEFINITION
EST 44 Green Apricot Fruit lambda Zap II Library Prunus armeniaca
cDNA clone ba001c13 3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CB819052 GI:29950859
Prunus armeniaca (apricot)
Prunus armeniaca
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Magnoliophyta; Magnoliopsida; eucoityledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
1 (bases 1 to 454)
Grimplet, J., Romieu, C., Audergon, J.M., Albagnac, G., Lambert, P.,
Bouchet, J.P. and Terrier, N.
High Throughput Detection of Isogenes among 5724 3' EST from
Apricot Fruit (Prunus armeniaca)
Unpublished (2003)
Contact: Audergon JM
Unité de génétique et amélioration des fruits et légumes
Institut National de la Recherche Agronomique
Domaine Saint-Maurice Bp 94 81413 Montfavet cedex
Tel: 00-33-(0)4-32-72-26-68
Fax: 00-33-(0)4-32-72-26-62
Email: audergon@avignon.inra.fr
Seq primer: 17

FEATURES
Location/Qualifiers


```

source
1..454
/organism="Prunus armeniaca"
/mol_type="mRNA"
/cultivar="Bergeron"
/db_xref="taxon:36596"
/clone="ba001c13"
/dev_stages="Green stage"
/clone_lib="Green Apricot Fruit Lambda Zap II Library"
/note="Organ: Fruit; Vector: Lambda Zap II; Site 1: Eco
RI; Site 2: XhoI; Oriented library, construction described
in Molecular cloning and expression of a cDNA encoding
1-aminocyclopropane-1-carboxylate (ACC) oxidase from
apricot fruit (Prunus armeniaca cv. Bergeron) by
Mbeugie-Mbeugie D, Chahine H, Gomez RM, Gouble B, Audergon
JM, Souty M, Albagnac G, Fils-Lycaon B in Physiol Plant
105:294-303 1999"

ORIGIN
Query Match      18.3%; Score 32; DB 14; Length 454;
Best Local Similarity 65.3%; Pred. No. 32;
Matches 47; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Qy 9 AACTGCTGAAATGTTTGGCATGCTACTGACAGTAAAGTTTCCCAATCCCAAC 68
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 358 ATCTCTGTGACACGGGCTTGGCAAGATTTCAGAACTTCAGATTGATGCTTCCAA 299
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 69 TCTGTCTCTGCCA 80
    ||||| |||||
Db 298 TCTTCAAGCCA 287

RESULT 14
BE237161
LOCUS
DEFINITION
146328 MARC 4BOV Bos taurus cDNA 5', mRNA linear EST 25-APR-2001
BE237161
ACCESSION
BE237161.1 GI:9021879
VERSION
KEYWORDS
SOURCE
Bos taurus (cow)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bos;
1 (bases 1 to 553)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrkrug,S.C.,
Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
Chitko-McKown,C.G., Perlea,G., Holt,I., Karamycheva,S., Liang,F.,
Quackenbush,J. and Keefe,J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
PUBMED
11282978
COMMENT
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTGCTGACGAG
Plate: 46 row: H column: 9
Seq primer: ATTATGGTGACACTATAG.
Location/Qualifiers
1..553
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"

ORIGIN
Query Match      18.2%; Score 31.8; DB 9; Length 995;
Best Local Similarity 56.4%; Pred. No. 57;
Matches 57; Conservative 1; Mismatches 43; Indels 0; Gaps 0;

Qy 3 CGGCAAACTGCTGAAATGTTTGGCATGCTACTGACAGTAAAGTTTCCCAATC 62
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 222 CGCCAAATAACAGCATGTTGTTAACTCCCGAGTGGGGCTAGATTCCCATG 281
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 63 CTCAACTCTGCTGCCAGCTGATGAGGGAAGGAAGGA 103
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 4BOV"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from day 20 and day 40
embryos."

ORIGIN
Query Match      18.3%; Score 32; DB 10; Length 553;
Best Local Similarity 55.4%; Pred. No. 36;
Matches 62; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 40 CTGACAGTAAAGTTTCCCAATCCTCAATCTCTCTGCCAGCTGATGAGGGAAGGAAA 99
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 130 CACCAAGGAGGGTGGCCCTTCTGAGTCTTCTGCTCCAGGCCGCGGCCGCC 189
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 100 GGGATTACCTAGGGGTATGGGCGACCAATCTGAGTCCACCACTGACACAG 151
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 190 AGGAGGACTAGGGGTGCGGGGAGCACCTGCTGCCCTCTACTGACGAGG 241
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
AL570803
LOCUS
DEFINITION
AL570803 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
AL570803
ACCESSION
AL570803.2 GI:31292218
VERSION
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 995)
Li,W.B., Gruber,C., Jessee,J. and Pollayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:12924770.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9221.r for
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI022AA06NP1&cluster=9221.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI022AA06NP1.
FEATURES
Location/Qualifiers
1..995
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI022Yall"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoRV
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match      18.2%; Score 31.8; DB 9; Length 995;
Best Local Similarity 56.4%; Pred. No. 57;
Matches 57; Conservative 1; Mismatches 43; Indels 0; Gaps 0;

Qy 3 CGGCAAACTGCTGAAATGTTTGGCATGCTACTGACAGTAAAGTTTCCCAATC 62
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 222 CGCCAAATAACAGCATGTTGTTAACTCCCGAGTGGGGCTAGATTCCCATG 281
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 63 CTCAACTCTGCTGCCAGCTGATGAGGGAAGGAAGGA 103
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

us-09-808-388-5_copy_1_175.sept04.rst

Mon Sep 13 07:48:10 2004

Db 282 GTGACCTGTGACCTGTGCTCCCTGAGASAGGGAGGCCCGAGGSA 322

Search completed: September 11, 2004, 08:16:05
Job time : 2758 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 06:15:11 ; Search time 75 Seconds
(without alignments)
1294.885 Million cell updates/sec

Title: US-09-808-388-5_COPY_1_175
Perfect score: 175
Sequence: 1 cgcggcaaaactgctgaaa.....tccccagcctgtgctcac 175

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgm2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgm2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgm2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgm2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgm2_6/ptodata/2/ina/PCTUS_COMB.seq.*
6: /cgm2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31.2	17.8	420	US-09-547-435-17	Sequence 17, Appl
2	31.2	17.8	1441	US-09-547-435-13	Sequence 13, Appl
3	31.2	17.8	2236	US-09-547-435-5	Sequence 5, Appl
4	31.2	17.8	2604	US-09-547-435-23	Sequence 23, Appl
5	31.2	17.8	2701	US-09-547-435-1	Sequence 1, Appl
6	31.2	17.8	3384	US-09-547-435-29	Sequence 29, Appl
C 7	30.6	17.5	305	US-09-328-111-618	Sequence 618, App
C 8	30.6	17.5	2885	US-09-016-434-1143	Sequence 1143, Ap
9	30.4	17.4	1549	US-08-856-444-1	Sequence 1, Appl
10	30.2	17.3	340	US-09-833-381-1715	Sequence 1, Appl
11	30.2	17.3	1794	US-09-320-312D-988	Sequence 988, App
12	29.2	16.7	3111	US-09-014-969-12	Sequence 12, Appl
C 13	29	16.6	204	US-09-506-729-37	Sequence 37, Appl
C 14	29	16.6	1883	US-08-202-056-2	Sequence 2, Appl
C 15	29	16.6	1933	US-08-076-093A-1	Sequence 1, Appl
C 16	29	16.6	1933	US-08-410-451-1	Sequence 1, Appl
C 17	29	16.6	1933	US-08-410-455-1	Sequence 1, Appl
C 18	29	16.6	1933	US-08-418-919-1	Sequence 1, Appl
C 19	29	16.6	1933	US-08-410-453A-2	Sequence 1, Appl
C 20	29	16.6	1933	US-08-701-265-1	Sequence 2, Appl
C 21	29	16.6	1933	US-08-410-454A-2	Sequence 1, Appl
C 22	29	16.6	1933	US-08-284-586-1	Sequence 2, Appl
C 23	29	16.6	1933	US-08-410-456A-2	Sequence 2, Appl
C 24	29	16.6	1933	US-08-805-478-1	Sequence 1, Appl
C 25	29	16.6	1933	US-08-802-627A-1	Sequence 1, Appl
C 26	29	16.6	1933	US-08-801-238-1	Sequence 1, Appl
C 27	29	16.6	1933	US-08-801-228-1	Sequence 1, Appl

C 28 29 16.6 1933 3 US-09-104-296-1 Sequence 1, Appli
C 29 29 16.6 1933 4 US-09-023-655-1134 Sequence 1134, Ap
C 30 29 16.6 1933 5 PCT-US94-06380-1 Sequence 1, Appli
31 28.6 16.3 891 4 US-09-711-164-156 Sequence 156, App
32 28.6 16.3 3728 1 US-08-111-939-1 Sequence 1, Appli
C 33 27.6 15.8 364 4 US-09-621-976-17202 Sequence 17202, A
C 34 27.2 15.5 1662 4 US-09-543-681A-3937 Sequence 3937, Ap
C 35 27 15.4 557 4 US-09-702-705-918 Sequence 918, App
C 36 27 15.4 557 4 US-09-736-457-918 Sequence 918, App
C 37 27 15.4 557 4 US-09-614-124B-918 Sequence 918, App
C 38 27 15.4 557 4 US-09-671-325-918 Sequence 918, App
C 39 27 15.4 3021 4 US-09-556-877-182 Sequence 182, App
C 40 27 15.4 3021 4 US-09-598-419-182 Sequence 182, App
C 41 27 15.4 3935 4 US-09-060-482-1 Sequence 1, Appli
42 27 15.4 3935 4 US-09-188-930-218 Sequence 218, App
43 26.8 15.3 1001 3 US-09-312-283C-218 Sequence 218, App
44 26.8 15.3 1001 4 US-09-188-930-30 Sequence 30, Appl
45 26.8 15.3 1015 3

ALIGNMENTS

RESULT 1
US-09-547-435-17
; Sequence 17, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-547-435-17

Query Match 17.8%; Score 31.2; DB 4; Length 420;
Best Local Similarity 55.6%; Pred. No. 0.14; Mismatches 0; Gaps 0;
Matches 60; Conservative 0; Indels 48; Indels 0; Gaps 0;
QY 68 CTCTGTCCTGCCAGCTGATGAGGGGAGGAGGAGGATTACCTAGGGGTATGGGCGACAA 127
Db 36 CTCTGCCAGACGCTGCTGTCACAGTGGGAGCATGACTTTGGGGCTTGGATGCCAA 95
QY 128 TCTGTAGTCCACCACTGACCGCCATCCCGAGCTTGTGCTCAC 175
Db 96 TGTTCATCATCATGAGGAGCGCCGCCAGACCCAGACGAGGAGGACAC 143

RESULT 2
US-09-547-435-13
; Sequence 13, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435

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; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 1441
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-547-435-13

Query Match      17.8%; Score 31.2; DB 4; Length 1441;
Best Local Similarity 55.6%; Pred. No. 0.25; Indels 0; Gaps 0;
Matches 60; Conservative 0; Mismatches 48;

QY      68  CTCTGTCCTGCCAGCTGATGAGGGGAGGAAAGGGATTACCTAGGGGTATGGCGACCAA 127
Db      492  CTCTGCCAGCAGCGTGTCTCAACAGTGGGCAGCATGACTTTTGGGGCCTGGATGCCAA 551

QY      128  TCTGTAGTCCACCACTGACGACGCCCATCCCCAGCGCTTGTGCCTCAC 175
Db      552  TGTCTCATCATCATGAGCGAGCGCCCCACCCAGACCAAGGGGACCAC 599

RESULT 3
US-09-547-435-5
; Sequence 5, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2236
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-547-435-5

Query Match      17.8%; Score 31.2; DB 4; Length 2236;
Best Local Similarity 55.6%; Pred. No. 0.3; Indels 0; Gaps 0;
Matches 60; Conservative 0; Mismatches 48;

QY      68  CTCTGTCCTGCCAGCTGATGAGGGGAGGAAAGGGATTACCTAGGGGTATGGCGACCAA 127
Db      1287  CTCTGCCAGCAGCGTGTCTCAACAGTGGGCAGCATGACTTTTGGGGCCTGGATGCCAA 1346

QY      128  TCCTGAGTCCCACTGACCAACGCCCATCCCCAGCGCTTGTGCCTCAC 175
Db      1347  TGTCTCATCATCATGAGCGAGCGCCCCACCCAGACCAAGGGGACCAC 1394

RESULT 4
US-09-547-435-23
; Sequence 23, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435

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; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 3384
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-547-435-29

Query Match      17.8%; Score 31.2; DB 4; Length 3384;
Best Local Similarity 55.6%; Pred. No. 0.36;
Matches 60; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 58 CTCCTGCTGCGAGCTGATGAGGGGAGGAAAGGGATTAACCTAGGGGTATGGCGGACCAA 127
Db 2250 CTCCTGCCAGCAGCTGCTGTCAACAGTGGCGAGCATGACTTTGGGCTGTGATGCCCHA 2309

QY 128 TCTTGAGTCCCAACTGACACAGCGCCATCCCGAGCCCTTGTCCCTCAC 175
Db 2310 TGCTCATCATCTATGAGGAGCGCCCGCCACCCCGAGACCAAGGGGAGCCAC 2357

RESULT 7
US-09-328-111-618/c
; Sequence 618, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
; APPLICANT: Endege, Wilson O.
; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Derti, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/328,111
; CURRENT FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: US 60/098,801
; EARLIER FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 618
; LENGTH: 305
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-328-111-618

Query Match      17.5%; Score 30.6; DB 3; Length 305;
Best Local Similarity 56.4%; Pred. No. 0.2;
Matches 57; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 3 CGCAAAATCGCTGAAATGTTTGGCATCAGTACTGACACGTAAGTTTCCCAATC 62
Db 217 CGCAAAATACACAGATGTTGTGAACATCCCCAGTGGGGCTAGAAATTCCTCATG 158

QY 63 CTCACCTCTGCTGCGAGCTGATGAGGGGAGGAAAGGGA 103
Db 157 GTGACCTGTGACCTGTCTCTCCGTGAGACAGAGGGGAGGCCAGGCA 117

RESULT 8
US-09-016-434-1143/c
; Sequence 1143, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
```

```
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1143:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2885 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENEBANK
; CLONE: g1478280
US-09-016-434-1143

Query Match      17.5%; Score 30.6; DB 4; Length 2885;
Best Local Similarity 56.4%; Pred. No. 0.55;
Matches 57; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 3 CGCAAAATCGCTGAAATGTTTGGCATCAGTACTGACACGTAAGTTTCCCAATC 62
Db 2633 CGCAAAATACACAGATGTTGTGAACATCCCCAGTGGGGCTAGAAATTCCTCATG 2574

QY 63 CTCACCTCTGCTGCGAGCTGATGAGGGGAGGAAAGGGA 103
Db 2573 GTGACCTGTGACCTGTCTCTCCGTGAGACAGAGGGGAGGCCAGGCA 2533

RESULT 9
US-08-856-444-1
; Sequence 1, Application US/08856444
; Patent No. 5959081
; GENERAL INFORMATION:
; APPLICANT: Lecka-Czernik, Beata
; TITLE OF INVENTION: No. 5959081el Zinc Binding LIM Protein S2-6
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Benjamin Aaron Adler, Ph.D. J.D.
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
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;; TITLE OF INVENTION: ENCODING THEM
;; NUMBER OF SEQUENCES: 32
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genetics Institute, Inc.
;; STREET: 87 CambridgePark Drive
;; CITY: Cambridge
;; STATE: MA
;; COUNTRY: U.S.A.
;; ZIP: 02140
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/014,969
;; FILING DATE:
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sprunger, Suzanne A.
;; REGISTRATION NUMBER: 41,323
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 498-8284
;; TELEFAX: (617) 876-5851
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3111 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
US-09-014-969-12

Query Match 16.7%; Score 29.2; DB 2; Length 3111;
Best Local Similarity 57.8%; Pred. No. 1.8;
Matches 52; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 72 GTCTGCGAGCTGATGAGGGAAGGATTACCTAGGGTATGGCGGACCAATCCCT 131
DB 957 GTCTGCGGCTGATGACGAGCTTGATAGAGACTAGGCTGAGCTGTCCCAATCCC 1016
QY 132 GAGTCCACCACTGACACGCCCATCCCCA 161
DB 1017 CATGCGGGATCTTCCACACCCGCTCTCA 1046

RESULT 13
US-09-506-729-37/c
; Sequence 37, Application US/09506729
; Patent No. 6365352
; GENERAL INFORMATION:
; APPLICANT: Yerramilli, Subrahmanyam V.
; APPLICANT: Prashar, Yatindra
; APPLICANT: Newberger, Peter
; APPLICANT: Goguen, Jon
; APPLICANT: Weissman, Sherman M.
; TITLE OF INVENTION: A PROCESS TO STUDY CHANGES IN GENE EXPRESSION IN
; FILE REFERENCE: 44921-5016-US
; CURRENT APPLICATION NUMBER: US/09/506,729
; EARLIER FILING DATE: 2000-02-18
; EARLIER APPLICATION NUMBER: PCT/US98/17284
; EARLIER FILING DATE: 1998-08-21
; EARLIER APPLICATION NUMBER: 60/056,844
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 204
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-506-729-37

Query Match 16.6%; Score 29; DB 4; Length 204;
Best Local Similarity 57.0%; Pred. No. 0.63;
Matches 53; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 4 GGCAAACTGCTGAAATGTGTTTGGCATGACGTAAGGTTTCCCAATCC 63
DB 194 GGAACATCTGCTGCCCAATGAGTGTGGTGCACATGGCTTTCTAGGATGCTGATGC 135
QY 64 TCAACTCTGCTGCCAGCTGATGAGGGGAAGG 96
DB 134 TGCAGCCAGCTTGAAGCTGCAGAGGGGAAGG 102

RESULT 14
US-08-202-056-2/c
; Sequence 2, Application US/08202056
; Patent No. 5440021
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Hebert, Caroline
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Lee, James
; TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,056
; FILING DATE: 25-FEB-1994
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1883 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-202-056-2

Query Match 16.6%; Score 29; DB 1; Length 1883;
Best Local Similarity 57.0%; Pred. No. 1.7;
Matches 53; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 4 GGCAAACTGCTGAAATGTGTTTGGCATGACGTAAGGTTTCCCAATCC 63
DB 1865 GGAACATCTGCTGCCCAATGAGTGTGGTGCACATGGCTTTCTAGGATGCTGATGC 1806
QY 64 TCAACTCTGCTGCCAGCTGATGAGGGGAAGG 96
DB 1805 TGCAGCCAGCTTGAAGCTGCAGAGGGGAAGG 1773

RESULT 15

US-08-076-093A-1/c
; Sequence 1. Application US/08076093A
; Patent No. 5543503
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: Antibodies to Human Pf4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/076,093A
; FILING DATE: 11-Jun-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/67211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1933 nucleotides
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-08-076-093A-1

Query Match 16.8%; Score 29; DB 1; Length 1933;
Best Local Similarity 57.0%; Pred. No. 1.7;
Matches 53; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 4 GGCARAACTGCCTGAATGTTTGGCATCAGCTACTGACACGTAAGGTTTCCCAATCC 63
Db 1915 GGAACATCTGCTGCCAATGGACTGGTGGCTGCACATGGCTTCTAGGGATGCTGATGC 1856
QY 64 TCAACTCTGTCTGCCAGCTGATGAGGGGAAG 96
Db 1855 TGCAGCCGACCTTGGAGCTGCAGAGGGGAAG 1823

Search completed: September 11, 2004, 08:17:25
Job time : 76 secs